

Table 8

5318	db mining	Hs.75969	AI568695	4532069	proline-rich protein with nuclear targeting signal (B4-2), mRNA /cds=(113,1098)	-1	AAAACCATTCAGCTTAATGCCCTTAA TTTAAATGCCAACAAATTGGGG
5319	Table 3A	NA	AI568725	4532099	th15a01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118312 3', mRNA sequence	-1	TGCAACCTCTTAAAAATGTGGGCTAC TGGAGATCATGCCACTGCACTCCA
5320	Table 3A	Hs.159014	AI568751	4532125	th15d09.x1 cDNA, 3' end /clone=IMAGE:2118353 /clone_end=3'	-1	AGCTCAGATGGGTCCCCAAAAGAGG CATAGGAAAGCGCGACCTCACTGCC
5321	db mining	Hs.174242	AI568753	4532127	th15e04.x1 cDNA, 3' end /clone=IMAGE:2118366 /clone_end=3'	-1	CAAATAAAAAGGCTGGGGCCAAAGG TGGGCACCAAAAGTCCTCTATGTG
5322	Table 3A	NA	AI568755	4532129	th15f03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2118365 3', mRNA sequence	-1	TGCAGCTCCCATTTCTGAGCGTCTA CCAGGTACTAGGAGAACTCTTACA
5323	db mining	Hs.327876	AI568771	4532145	th15h04.x1 cDNA, 3' end /clone=IMAGE:2118391 /clone_end=3'	-1	ATTATCCTTTTCCCAGGAAGCCCTC GGCCCCAAAAGGGAAACAGTTT
5324	db mining	Hs.179070	AI568773	4532147	th15h09.x1 cDNA, 3' end /clone=IMAGE:2118401 /clone_end=3'	-1	CATGAGCCCAGGGGTTTCATGACAAA CATTACTAGCATGTCCAACGCCC
5325	Table 3A	NA	AI569898	4533272	tr57c12.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:222422 3' similar to gb:D16234 PROBABLE PROTEIN DISULFID	-1	GCCCGGTTTATGGAAAAACAGGAC CAGTTTATGTTTGGGGTTTGGGAA
5326	Table 3A	Hs.92448	AI570295	4533669	EST380664 cDNA	-1	GCTTGGTACTGTCACTAGTATTACAA ATTTTCATGGAATCGAAGAGCAAC
5327	Table 3A	Hs.5637	AI570531	4533905	60298983F1 cDNA, 5' end /clone=IMAGE:5141013 /clone_end=5'	-1	TTTTCTCCCTCTCTTCCCTTCCAC GAAGTCAATACCAAGTAACCTTGG
5328	Table 3A	Hs.14623	AI571519	4534893	interferon, gamma-inducible protein 30 (IFI30), mRNA /cds=(40,951)	-1	AAGCCCAGATACAAAAATCCACCC CATGATCAAGAATCCTGCTCCACT
5329	db mining	Hs.8882	AI572757	4536131	tu43c07.x1 cDNA, 3' end /clone=IMAGE:2253804 /clone_end=3'	-1	CATGTGTTGACTCTGTAATGGATTAT GTAGCCCACTTCAGTCTGCAAT
5330	Table 3A	Hs.230430	AI579979	4564355	tq45a01.x1 cDNA, 3' end /clone=IMAGE:2211720 /clone_end=3'	-1	AGGGGTGTCCCTTTTCCCTTCATGT AAAATTCTAACTGGGGCTACCAGT
5331	Table 3A	NA	AI581199	4565575	tl94h10.x1 NCI_CGAP_Co14 cDNA clone IMAGE:2154787 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCCTACGTTT
5332	Table 3A	Hs.327922	AI581383	4565759	to71c02.x1 cDNA, 3' end /clone=IMAGE:2183714 /clone_end=3'	-1	TGAAGAACTGCCCTTTCTGTGATGT TTTTGAATACTACCAACAGCCAA
5333	Table 3A	Hs.229918	AI581732	4567629	ar74f03.x1 cDNA, 3' end /clone=IMAGE:2128349 /clone_end=3'	-1	CTTCTAGCCCTAAGTTTGGCCTTTG GGTGGCTCCAAAAAGGATTAGGTT
5334	Table 3A	Hs.292553	AI582954	4568851	tr98e07.x1 cDNA, 3' end /clone=IMAGE:2227140 /clone_end=3'	-1	TCCCCCTCGTTTTGTAGGGTTTGTAC ATAATAAAACAATGGGGTGGGGCC
5335	Table 3A	Hs.340925	AI590337	4599385	wh96a06.x1 cDNA, 3' end /clone=IMAGE:2388562 /clone_end=3'	-1	TGTTAAGTGTGAGTTTTCTGAACCC TAGCAGAAGGACTTTTAATGTTT
5336	Table 3A	Hs.101617	AI597917	4606976	601513709F1 cDNA, 5' end /clone=IMAGE:3914786 /clone_end=5'	-1	AGTTCACCTGCTGTCTCTTACCTT GATTAAATGCCTATGCATGTAATT
5337	db mining	Hs.13646	AI611245	4620412	601287348F1 cDNA, 5' end /clone=IMAGE:3621754 /clone_end=5'	-1	AGTTCGTGTTGTGAATCTGGTGCTGG TTCCCTGGGCATATGATTCTGTG
5338	Table 3A	NA	AI619574	4628700	ty50c09.x1 NCI_CGAP_UI2 cDNA clone IMAGE:2282512 3' similar to gb:M23613 NUCLEOLAR PHOSPHOPROTEIN B	-1	CCCCCTTGCTTGGTTTTAAGTAGGTA TGGAATGTTATTATAGGCCATAGT
5339	db mining	Hs.340564	AI625119	4650050	ts47b12.x1 cDNA, 3' end /clone=IMAGE:2231711 /clone_end=3'	-1	TCAGTGTAACATAATTAGGCCGTGA GTTTTTGCTCTTACTCCAGGTTT
5340	Table 3A	Hs.188365	AI625368	4650299	ts37c10.x1 cDNA, 3' end /clone=IMAGE:2230770 /clone_end=3'	-1	TGTAACTTGTTTTAACAACTCTTTTC AACATTTTGGCCGGGGTATTCCC
5341	Table 3A	Hs.278554	AI627495	4664295	chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds=(111,662)	-1	TGCTGAAAGTGGTCCCAAGGGGTA CTAGTTTTTAAGCTCCCAACTCCCC
5342	Table 3A	Hs.171262	AI628893	4665693	ty95h02.x1 cDNA, 3' end /clone=IMAGE:2286867 /clone_end=3'	-1	TTCCCAAGTTGCCACAGACCGTTTATA TGAAGAAATGCTAAAGAAGTTCCC
5343	Table 3A	NA	AI628930	4665730	ty40d03.x1 NCI_CGAP_UI2 cDNA clone IMAGE:2281541 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCCTACGTTT
5344	db mining	Hs.264154	AI630176	4681508	ad05a03.r1 cDNA /clone=ad05a03-(random)	-1	AGTTCTAAAGCCGGGAATTCCTAAGG ATATACTAAATGAGATTATGTGTGG

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5345	Table 3A	Hs.340604	AI631850	4683180	wa36h07.x1 cDNA, 3' end /clone=IMAGE:2300221 /clone_end=3'	-1	GCCTGGGGGAGGAGAAGTCCCTTCC CATTCCAGCTCGATCAATCTTGCTG
5346	Table 3A	Hs.256729	AI634652	4685982	wx27c05.x1 cDNA, 3' end /clone=IMAGE:2544872 /clone_end=3'	-1	GGAGTAGAGAGAGTCTTGCTACATGC GGGAAGTAGAATTACATCACTGCG
5347	Table 3A	Hs.319825	AI634972	4686302	602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5'	-1	AAGAAGTTTCATTGATATCCACTGGT CACATCATACCTGCTATAGGCGA
5348	Table 3A	Hs.176920	AI638800	4691034	tt32e01.x1 cDNA, 3' end /clone=IMAGE:2242488 /clone_end=3'	-1	TGCTTCAAGCACAGGATTATGGAAT AGTTGGCAAATTAACAAACATGCT
5349	Table 3A	Hs.197028	AI650871	4734850	602643870F1 cDNA, 5' end /clone=IMAGE:4774817 /clone_end=5'	-1	CGGCAGCCTTATGGAATGAGTTTCTT GTCATGAATGTTGCCCAAGCT
5350	Table 3A	Hs.4283	AI651212	4735191	602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5'	-1	ACAGTTACTTTGGAGCTGCTAGACTG GTTTTCTGTGTTGGTAAATGCGT
5351	db mining	Hs.203064	AI651922	4735901	hy16b12.x1 cDNA, 3' end /clone=IMAGE:3197471 /clone_end=3'	-1	TGTGAAGAATCCCTACCATTAAATACC CTGGGTGGGATAAATAAAATGGG
5352	Table 3A	Hs.195378	AI653766	4737745	ty01b06.x1 cDNA, 3' end /clone=IMAGE:2277779 /clone_end=3'	-1	CCCAAAATTTGTTTAAAGTCCGACTT CCAAAGGGGCCAATAAAAGGG
5353	db mining	Hs.111941	AI660405	4763975	qd92a04.x1 cDNA, 3' end /clone=IMAGE:1736910 /clone_end=3'	-1	CACCGCCTCTGCCTCCGCTCTTCCA CTGGAGAGCCGAGGTCAAAGGTC
5354	Table 3A	Hs.200442	AI669591	4834365	tw34b09.x1 cDNA, 3' end /clone=IMAGE:2261561 /clone_end=3'	-1	CCCTCACCTAGCAGTACTACCACAAT AATGCTATCATGGTGCCAGGGAAT
5355	Table 3A	Hs.101150	AI672433	4852164	Homo sapiens, clone IMAGE:4054156, mRNA, partial cds /cds=(0,526)	-1	TCTCCTTCCCCATTGGGCCCGCTTTA TCAATTGCTGTTTTGTTTGT
5356	Table 3A	Hs.341178	AI678004	4888186	xa30a04.x1 cDNA, 3' end /clone=IMAGE:2568270 /clone_end=3'	-1	TTTTATCTTTCTGGTGGGGGTGTG GTGGTGGTGAGAGGACCTAAAAA
5357	Table 3A	Hs.324507	AI678099	4888281	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(182,2056)	-1	CGCCAGAGGTCAGAACATGTCTATTT TGAATTGGATCGTTACAAATGAGC
5358	Table 3A	Hs.178784	AI681868	4892050	602587746F1 cDNA, 5' end /clone=IMAGE:4716442 /clone_end=5'	-1	GCAGGCACCTGACATTTTGTAGCAAAG ACGTGATGTTATGAGATAAATATC
5359	Table 3A	Hs.90744	AI684022	4895316	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds=(0,1268)	-1	TTCTGACACGATTACACAACGAGGCT TTAATGCCATTTGGGTAGGTGAGC
5360	db mining	Hs.328323	AI684369	4895663	tc96e09.x1 cDNA, 3' end /clone=IMAGE:2074024 /clone_end=3'	-1	TTTTAAAGGGGAGGGGCCGGGTTT GGTCCCCGGTCCCAAGGTAAAGTT
5361	Table 3A	Hs.58774	AI684437	4895731	Homo sapiens, Similar to zinc finger protein 175, clone MGC:12651 IMAGE:4301632, mRNA, complete cds /cds=(367,522)	-1	GAGTGAGAAGAGGCTTTTAAGGACCA TGTGAAGAGGCTTTTAACACTTT
5362	db mining	Hs.182817	AI684847	4896141	602290551F1 cDNA, 5' end /clone=IMAGE:4385293 /clone_end=5'	-1	GGGTTGGGATAAACTGCTTAGATGTT TGCCTACTTGTCCAGTGAAATTAC
5363	Table 3A	NA	AI688560	4899854	wd39f08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA sequence	-1	ACTGAAAAGTTGAAAGACTTTTGCAG TGAACATTATATAACTCCCCGCT
5364	Table 3A	Hs.201789	AI693179	4970519	MR1-CI0181-061100-001-a01 cDNA	-1	ATTCATAGGTAGTCCCAGAGAGAGT ACAAGCTCTGACTCATATGGCAGT
5365	literature	Hs.202407	AI697497	4985397	we14b06.x1 cDNA, 3' end /clone=IMAGE:2341043 /clone_end=3'	-1	ACATGTTACCTGGAGTAGCTGTGTCA ACAGATTAATATGGAATGCTACTA
5366	Table 3A	Hs.177708	AI697756	4985658	602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5'	-1	TGGTTCCTGTGCTCACCATAGGGCTG GTGTACATTGGGCCATTAATAAAC
5367	Table 3A	Hs.206654	AI700738	4988638	EST368531 cDNA	-1	ACAGATCCCTATTGCCAGACACATCA TTCTCTCCATCCAGAAAGCAAACA
5368	Table 3A	Hs.80887	AI701165	4989065	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835)	-1	TCTGGGAAAGACATTTTAACTGCT GACTTCACCTGCAAAATCTAACAG
5369	Table 3A	Hs.102793	AI707589	4997365	RST17769 cDNA	-1	AGTCACGATAAACCTGGTCACCTGAA AATTGAAATTGAGCCACTTCTTG
5370	Table 3A	Hs.309433	AI707809	4997585	as28g09.x1 cDNA, 3' end /clone=IMAGE:2318560 /clone_end=3'	-1	AACTGGCGGCCCAACAAACAGTG GGTTAAATGGGTCCCTGGGTGACAT
5371	Table 3A	Hs.107369	AI707896	4997672	as34a10.x1 cDNA, 3' end /clone=IMAGE:2319066 /clone_end=3'	-1	AGTGTTCCTCCACATCTAAAGAAAG CCCATTTTGAAACTGGATACTGCA
5372	Table 3A	Hs.176430	AI708327	4998103	at04c02.x1 cDNA, 3' end /clone=IMAGE:2354114 /clone_end=3'	-1	CCCAGGTGGCCCTCTCCATCAGAT GTTATTGCTCTTCCCATTATTTA

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5373	Table 3A	Hs.300710	AI709236	4999012	RC0-MT0059-200600-021-g05 cDNA	-1	AAGATGCCTAAGCGTTAACCAAGGTGA AACAGGGGTGGGAGAGAGAAAGAA
5374	Table 3A	Hs.297184	AI720536	5037792	601502712F1 cDNA, 5' end /clone=IMAGE:3904539 /clone_end=5'	-1	GTCATACACCTATCCCCCATTTTCTT CCTATCCCTCAACCCGGACATCAT
5375	Table 3A	Hs.313929	AI733018	5054131	oh60h01.x5 cDNA, 3' end /clone=IMAGE:1471441 /clone_end=3'	-1	GCAGGTGGCAGAATGGGGTGCATGA AGGTTTCTGAAAATTAACACTGCTT
5376	Table 3A	Hs.310333	AI735206	5056730	at07f03.x1 cDNA, 3' end /clone=IMAGE:2354429 /clone_end=3'	-1	ACAGAGAGGCAGCATTTGTTTCCAG TTAAATTTGACCTCACTGTGATT
5377	Table 3A	Hs.277201	AI740667	5108955	wg07b07.x1 cDNA, 3' end /clone=IMAGE:2364373 /clone_end=3'	-1	CCCCCTTTTGTGTGGTTTTATATTGG AACCCCTTTTCTTTGGAACCTA
5378	Table 3A	Hs.204656	AI741246	5109534	wg26g09.x1 cDNA, 3' end /clone=IMAGE:2366272 /clone_end=3'	-1	CTGACCCCTTCTCACCCTGCCAAC AGTGGTGGCATATATCACAAATGG
5379	Table 3A	Hs.299883	AI742850	5111138	hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769)	-1	TGTTTTACCTCACTGTGGACATACAT TCCAAGCTTTTCAACTCTAGGAG
5380	Table 3A	Hs.6187	AI745230	5113518	wg10e05.x1 cDNA, 3' end /clone=IMAGE:2384704 /clone_end=3'	-1	CAGAACATGCCCAAAGAGCCTATAT CTTGCTGCTGGGAAATGTAAAGCA
5381	Table 3A	Hs.293842	AI748827	5127091	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	CAAACACCCGGCAGTTGAAAGGAAAA GGACGGGGAATGTGATGGAAGAGAG
5382	Table 3A	NA	AI749435	5127699	at24b04.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2356015 3' similar to gb:X55715 40S RIBOSOMAL PRO	-1	CCCCCTCCCTGCCCGGCTGAGCTTT GGGGAACCCAAAAATTAGATTTTGC
5383	Table 3A	Hs.204929	AI749444	5127708	at24c03.x1 cDNA, 3' end /clone=IMAGE:2356036 /clone_end=3'	-1	CCCAAATCCAAGGACCAATGCTGTG TAAACAAGGGGTAAAGGGCTAAA
5384	Table 3A	Hs.205071	AI760018	5175685	wh83b02.x1 cDNA, 3' end /clone=IMAGE:2387307 /clone_end=3'	-1	ACTCCACCAAGACTGTGAAGTCCACC GGGGTAGGAAGCATATTTTACTCA
5385	Table 3A	Hs.160951	AI760020	5175687	wh83b05.x1 cDNA, 3' end /clone=IMAGE:2387313 /clone_end=3'	-1	GAGAACTCGTTTCAAGGAAGTCTGATG TTTCGGGGACCAAGCCCGCCAG
5386	Table 3A	Hs.340921	AI760026	5175693	wh83c05.x1 cDNA, 3' end /clone=IMAGE:2387336 /clone_end=3'	-1	CCAGCGAATTTCCAGCTTTTGAAACT CAGATTTCCCTTTTCCGACCCAGGT
5387	Table 3A	Hs.26873	AI760224	5175891	wh62g06.x1 cDNA, 3' end /clone=IMAGE:2385370 /clone_end=3'	-1	GATGCGCGGCAAGAAATGTACCTGTA GATGTGTACATACCACAGTGCTGTA
5388	Table 3A	Hs.14373	AI760353	5176020	yx26h11.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5'	-1	TTTATCTCAGAATCTTGATGAAGTCTG AAATGACCCCTGATGGGGGCATG
5389	db mining	Hs.204598	AI760374	5176041	wh87d12.x1 cDNA, 3' end /clone=IMAGE:2387735 /clone_end=3'	-1	GGCCCCCTGTCCTTACCTGTTTTCGG CCCCCTTAATTTTTTAACCCCGGG
5390	db mining	Hs.283496	AI760389	5176056	wh87f08.x1 cDNA, 3' end /clone=IMAGE:2387751 /clone_end=3'	-1	GTCACAGTGTAGACACATGGTGCTTC CATAGTGAGTAGAATATCCATTGT
5391	db mining	Hs.340927	AI760556	5176223	wi10d09.x1 cDNA, 3' end /clone=IMAGE:2389841 /clone_end=3'	-1	GTGGCCTGGCCTGGCTCTCACAGAC CCAAGGCTCCGTGTAGAATATGTC
5392	db mining	Hs.205803	AI760674	5176341	wh96b04.x1 cDNA, 3' end /clone=IMAGE:2388559 /clone_end=3'	-1	GGATTGTGGCAGGAAGTGTTCCTTCCCT CCCAGCCTAAATTTTTCTGTGTT
5393	db mining	Hs.283497	AI760699	5176366	7f34c12.x1 cDNA, 3' end /clone=IMAGE:3296566 /clone_end=3'	-1	AAACCCACACCTCAGTGAATTTAAAA GAGTAGATGTTTTAAAGACCCGGA
5394	db mining	Hs.264654	AI760835	5176502	wh96f11.x1 cDNA, 3' end /clone=IMAGE:2388621 /clone_end=3'	-1	TGCCATTTGGTATTTTTCTGAAACA TTACATAATAAGAATGCAGCATGC
5395	Table 3A	NA	AI760901	5176568	wi09h06.x1 NCI_CGAP CLL1 cDNA clone IMAGE:2389787 3', mRNA sequence	-1	GCCTGAAACCATCTGCCTTCTAGGA AGACAGCAATTCTGGAAGAGCAAG
5396	db mining	Hs.230931	AI760991	5176658	wh97b11.x1 cDNA, 3' end /clone=IMAGE:2388669 /clone_end=3'	-1	GGTGGTTCCCGAGCCCTTTTCCCTGG CCCTGGGTTGAAAAATTTGTTTTT
5397	db mining	Hs.328494	AI761029	5176696	wi10d06.x1 cDNA, 3' end /clone=IMAGE:2389835 /clone_end=3'	-1	AAAACCTTTCCGCCGGCTTAAAAATT ACCGGGGTTTGGTTTTATTGGTTT
5398	Table 3A	Hs.98531	AI761058	5176725	wi69b03.x1 cDNA, 3' end /clone=IMAGE:2398541 /clone_end=3'	-1	CTCCTTGGTGTATGCAACTGAGGAA CCTAATTGGCTGGGTGGGTGTTTC
5399	Table 3A	Hs.205452	AI761141	5176808	wh97g08.x1 cDNA, 3' end /clone=IMAGE:2388734 /clone_end=3'	-1	GTTTGTAAGAAACCTGCCACATTTG TTGAAAGTTAGAGCCATCACAGC

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5400	Table 3A	NA	AI761144	5176811	wh97h01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388721 3', mRNA sequence	-1	CTCTTGGCTGCTGGCCTTTTGTCTT GTCATGGCTCATTAGCTCCCTAAA
5401	db mining	Hs.328495	AI761468	5177135	wh98e07.x1 cDNA, 3' end /clone=IMAGE:2388804 /clone_end=3'	-1	CCAGGGGTTTTTAAATTTCTGAAGTT TTTGGGGCATTGTTGTTGTTGG
5402	Table 3A	Hs.80887	AI761622	5177289	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297, 1835)	-1	CCCCGCTTGCCTTTTATTTTCAAGACC CCAAGTATTACCAATATGTTACA
5403	Table 3A	Hs.289834	AI761924	5177591	wg58h03.x1 cDNA, 3' end /clone=IMAGE:2370293 /clone_end=3'	-1	GCCGAAGCTCACAGAGGCTAAGTTA CACGCTTAGGTGTTCTTATTCCTAC
5404	Table 3A	Hs.204610	AI762023	5177690	wh89f04.x1 cDNA, 3' end /clone=IMAGE:2387935 /clone_end=3'	-1	AACCAAGTTTATGATGCTGTAATAAA CCATGGCATTAAAGAGGGCAAGAG
5405	db mining	NA	AI762158	5177823	wh90e05.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388032 3' similar to gb:X64707 BREAST BASIC CONSERVED PR	-1	GGGTAAAGGAGGGCCGCTCCAAAAT TTTCTTTTTCCAGGAAGCCCTTG
5406	db mining	Hs.204771	AI762177	5177844	wh90g09.x1 cDNA, 3' end /clone=IMAGE:2388064 /clone_end=3'	-1	ATGCTGTGAGTGGTACACATGGCTGA GGTATGATCTGTTAAATATGTA
5407	Table 3A	Hs.205327	AI762557	5178224	wh92f07.x1 cDNA, 3' end /clone=IMAGE:2388229 /clone_end=3'	-1	TTCAATTAATTCCTCAACCAATACTGT CTGGCTTCCACCAACAGGAGCGG
5408	db mining	Hs.328503	AI762707	5178374	wh93d06.x1 cDNA, 3' end /clone=IMAGE:2388299 /clone_end=3'	-1	TGGTTTCTATTTTTAAAACTGGGTTA GGCCAAGGTTTGGGGTTCGCCCT
5409	db mining	Hs.204477	AI762719	5178386	wh93e10.x1 cDNA, 3' end /clone=IMAGE:2388330 /clone_end=3'	-1	CAACATTGCCTACCAAGTTGCAGTTCA TTAGCCCGCTCGCCCGCAGCATTG
5410	db mining	Hs.205815	AI762739	5178406	wh93g11.x1 cDNA, 3' end /clone=IMAGE:2388356 /clone_end=3'	-1	CCTTTGGGGTGGGGGCTTTTCTCTT TGGCCGGTCAATTAAGGTTTTT
5411	Table 3A	NA	AI762741	5178408	wh93h02.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388339 3', mRNA sequence	-1	CCCACTCCGGCTGTTTTAGAAGTTTT CCCGAATCCGTGATCCCTTACAA
5412	db mining	NA	AI762797	5178464	wi04c12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2389270 3' similar to TR:Q61655 Q61655 EUKARYOTIC TRANSLA	-1	AATGGGCAAAATTTTACCCAAAACCTTA AGCTTGCTATTCCGTTTGAGGCA
5413	Table 3A	Hs.333513	AI762870	5178537	wi63c07.x1 cDNA, 3' end /clone=IMAGE:2397996 /	-1	GAAGGAGAGGCACACACAAATACAC ACACTCACACAAAACCTCAACAACCA
5414	db mining	Hs.204480	AI762931	5178598	wh94e08.x1 cDNA, 3' end /clone=IMAGE:2388422 /clone_end=3'	-1	GGATACCCCTTTATCCCAGGGAAT TTTTACCCTTTGGATGCCCTTAAA
5415	db mining	Hs.289836	AI762955	5178622	wh94g12.x1 cDNA, 3' end /clone=IMAGE:2388454 /clone_end=3'	-1	CAAATTACAACCTAAAAATACAGAA CATCAGCGGAGAAGACAGGAGAGC
5416	db mining	Hs.277238	AI763079	5178746	wh95a12.x1 cDNA, 3' end /clone=IMAGE:2388478 /clone_end=3'	-1	CTCCTCCCTTGGGTGGGACCTGGGT TGGGGGTTGATAGAAAAATTAACC
5417	Table 3A	Hs.173904	AI763121	5178788	wi06d12.x1 cDNA, 3' end /clone=IMAGE:2389463 /clone_end=3'	-1	GGTTAAACTAGATCCCTGCAAGGCCA TCACCTCCATTCCAAGTTGTACT
5418	Table 3A	Hs.190453	AI763206	5178873	wh95e09.x1 cDNA, 3' end /clone=IMAGE:2388520 /clone_end=3'	-1	AGTGGGTTATTTAGATCTTTTCTTG GGGTTCAGGTCACATAGCTTAAC
5419	db mining	Hs.283500	AI763225	5178892	UHH-BW1-anj-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082282 /clone_end=3'	-1	TGTTTGGGTATATTGTTTGGGTTTTG GGCCTAGGATGGGTGACTCAGGG
5420	Table 3A	Hs.130059	AI763262	5178929	wi66c04.x1 cDNA, 3' end /clone=IMAGE:2398278 /clone_end=3'	-1	GCCAGTGAATCTAGTTTTGGCTATTC TGTATTTTGTCAGTTTTTCCCAT
5421	db mining	Hs.328504	AI763414	5179081	wh92a11.x1 cDNA, 3' end /clone=IMAGE:2388188 /clone_end=3'	-1	AACCATTTTCCCCCGGAACCCGTTT TGCCTGGTTTCGGATTTTTTACCC
5422	Table 3A	Hs.36137	AI765153	5231662	hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0, 1043)	-1	CCGGGAAGCGGGGTACTGGCTGTGT TTAATCATTAAAGGTACCGTGTCCG
5423	db mining	Hs.340947	AI766625	5233134	wi01f06.x1 cDNA, 3' end /clone=IMAGE:2388995 /clone_end=3'	-1	TTTTCCCGCTCCCAAAATTCAGTGAT TACAGTTTTTGAAACAGAACGGG
5424	Table 3A	NA	AI766638	5233147	wi02a10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2389050 3', mRNA sequence	-1	TACGAGAAGTCAGGAAGTTTTGAAAT GGCAGTGACAGGAGACGGGGGAAG
5425	db mining	Hs.210276	AI766656	5233165	wi02d04.x1 cDNA, 3' end /clone=IMAGE:2389063 /clone_end=3'	-1	AAGGGCAGGCAAAATCAATTAATAATTA GCCGTAAACAACACCTCGGGGGTG
5426	Table 3A	Hs.223935	AI766706	5233215	wi02g11.x1 cDNA, 3' end /clone=IMAGE:2389124 /clone_end=3'	-1	AGTACACGGCCCTCAAAAGTTATATG TGCTGAATGTAACCTACTTAGCGA

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5427	Table 3A	Hs.89104	AI766963	5233472	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAACAACTCTTCTCAACATTT TGCCAGGTATTCTACTGTAACCA
5428	Table 3A	Hs.209511	AI768880	5235389	wh71e04.x1 cDNA, 3' end /clone=IMAGE:2386206 /clone_end=3'	-1	CTTCTCCACCTCGGCCAGGTATAGG GCCAGCTTCTCGTCTCTGGGATCCG
5429	Table 3A	Hs.203594	AI796317	5361780	uncharacterized gastric protein ZA43P mRNA, partial cds /cds=(0,134)	-1	GCCAGGTCATTGTATAGGGAGTAAGA TGAAGGTGAATTCAGCTAGTTG
5430	Table 3A	Hs.230939	AI796419	5361882	wj17f02.x1 cDNA, 3' end /clone=IMAGE:2403099 /clone_end=3'	-1	TGTGTTTTGTTTTCTGGTCCCAGGG CACCGTTTGTTTTGTGAACCTCCTC
5431	db mining	Hs.291079	AI797561	5363033	602437732F1 cDNA, 5' end /clone=IMAGE:4555638 /clone_end=5'	-1	CATGGCTCTAAAATTGGAATTAACCTT CTCTTGCCCTAAGAGCTGCTTGT
5432	Table 3A	Hs.159577	AI797788	5363260	wh78b11.x1 cDNA, 3' end /clone=IMAGE:2386845 /clone_end=3'	-1	GCTGGTGGGAAGTTGAGCCATGTTTA TCTCTAGTGGAATCCTTACCTTGT
5433	db mining	Hs.207473	AI797813	5363370	wh79c04.x1 cDNA, 3' end /clone=IMAGE:2386950 /clone_end=3'	-1	CATGTTTACACAAATTCCTTCAAAGC CCCTTAACATGGGGCCGGGCCCC
5434	db mining	Hs.171110	AI797852	5363409	7e88g03.x1 cDNA, 3' end /clone=IMAGE:3292276 /clone_end=3'	-1	ACCCTAATAGCTAGGCTGGGTATATT TTCAAAGTGTAAGCGAAACCCACG
5435	db mining	NA	AI797901	5363296	wh78f12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386895 3' similar to contains Alu repetitive element, m	-1	CAGTTGGCCTCCTACAATTGGGAATT CTACCAAGCTCCAAGTTGACCTGG
5436	db mining	Hs.226571	AI797918	5363311	DKFZp434G046_s1 cDNA, 3' end /clone=DKFZp434G046 /clone_end=3'	-1	GGATCCCCGACAAAGGCTTGATGTGT ACTTGAAGTGAGCAAAGGGTTTTC
5437	db mining	Hs.223520	AI797988	5363460	wh80a02.x1 cDNA, 3' end /clone=IMAGE:2387018 /clone_end=3'	-1	GGGTGGGAGACAGGCTAATCCTTTTC CCCTTGTTTTCCACGCTTTTATGAC
5438	db mining	Hs.207062	AI798027	5363499	wh80e09.x1 cDNA, 3' end /clone=IMAGE:2387080 /clone_end=3'	-1	ACAACCTTCTTAATATATTAGAGACCC GCAGGAAACATTTAGTGGTGAAAC
5439	db mining	Hs.341012	AI798028	5363500	wh80f11.x1 cDNA, 3' end /clone=IMAGE:2387085 /clone_end=3'	-1	GTACATGTTTGTTGTGCTAAATTGCTC ATTTGGCAGTGATAGATTGAAAAAC
5440	db mining	Hs.229494	AI798100	5363583	wh81d01.x1 cDNA, 3' end /clone=IMAGE:2387137 /clone_end=3'	-1	GGGGGTCAAAGAGGTTACAAATGTA TGGGGGTATATTGAATGCTAAACAT
5441	db mining	Hs.328535	AI798101	5363584	wh81d02.x1 cDNA, 3' end /clone=IMAGE:2387139 /clone_end=3'	-1	GGGAGCCCGTTTTAGAAGGAAGGGC AAAAGTAGGGTTTTAACCCAAACG
5442	db mining	Hs.210307	AI798114	5363576	wh81c01.x1 cDNA, 3' end /clone=IMAGE:2387136 /clone_end=3'	-1	TCCGTCCCATTCCTCCCGGAAACAAAG GTTTTGAATTGGCCCGTAAAGGG
5443	Table 3A	Hs.209609	AI798144	5363616	wh81g12.x1 cDNA, 3' end /clone=IMAGE:2387206 /clone_end=3'	-1	ACGTCCTTATACAATGCACTGTTTGA TTTTTAAACAATACCTGAAGGGCT
5444	Table 3A	Hs.158989	AI799909	5365381	602666595F1 cDNA, 5' end /clone=IMAGE:4806358 /clone_end=5'	-1	ACTCAATACTCGGGAAGGCTTCACA TTTCTGGGACTCAGCATTATCCAA
5445	Table 3A	Hs.135167	AI802181	5367664	AV712376 cDNA, 5' end /clone=DCAAND12 /clone_end=5'	-1	TTGAGAGGCAACACTTAAACACTAGG GCTACTGTGGCATCTATGTAGACA
5446	Table 3A	Hs.195175	AI802547	5368019	mRNA for CASH alpha protein /cds=(481,1923)	-1	AGCCCTTTCTTGTTGCTGTATGTTTA GATGCTTTCCAATCTTTTGTACT
5447	Table 3A	Hs.25648	AI803065	5368537	tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880)	-1	GGGGTATGGTTAGTAATATCCACCA GACCTTCGATCCAGCAGTTTGGT
5448	Table 3A	Hs.301209	AI804629	5370101	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (MLLT10), mRNA /cds=(183,3266)	-1	AACAACAACAGCAAAATCCCTTAGT GCGTAACTTGAAATCCCTTCGGC
5449	db mining	Hs.209261	AI805106	5391760	tc90g10.x1 cDNA, 3' end /clone=IMAGE:2073474 /clone_end=3'	-1	TTGTAAGTGGGTGCATAAGAAGATCT CTTCAATTAAATGCCCCCGCTGGT
5450	Table 3A	Hs.187698	AI805111	5391765	cytomegalovirus partial fusion receptor mRNA, partial cds /cds=(0,1037)	-1	ATAATTAAGAAATCAGCCGTGTGCTT CTCAGCTTTGGGCTCCGAGACGTG
5451	Table 3A	Hs.167206	AI805131	5391785	602727149F1 cDNA, 5' end /clone=IMAGE:4866348 /clone_end=5'	-1	GTCAGTCTCCTCACCTGCCTCTGCTC CTCGCTTAGCCCATTGATTGCATC
5452	db mining	NA	AI805144	5391798	td11g08.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2075390 3' similar to gb:L24038_ma1 A-RAF PROTO- ONCOGENE	-1	GGGAAGAAGCCCGTGCCCCACCCA ATAAATGTTGGTTTTGGCCCTGATG
5453	db mining	NA	AI805257	5391750	tc90f09.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073449 3', mRNA sequence	-1	CAGAACTTCTGGCGAAGGCCATGTAA GAACTACTCCAAGGAGGAAGAGGC

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5454	Table 3A	NA	AI807278	5393844	wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence	-1	CTCTACCATAAGGCACTATCAGAGAC TGCTACTGGAGTGTATATTGGTT
5455	db mining	NA	AI808039	5394527	wf52h02.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2359251 3' similar to TR:Q62845 Q62845 NEURAL CELL	-1	ACTGCTACAGCTTAACCATTTGTTCCA AGCTAATTAATAATTACCTTTGGGGA
5456	Table 3A	Hs.87912	AI808931	5395497	EST379776 cDNA	-1	CAATTGTGATTGGAAGGTTTAACTG GGTCTGCCAGATGTTTACGAATA
5457	db mining	Hs.209989	AI809181	5395747	wh75d05.x1 cDNA, 3' end /clone=IMAGE:2386569 /clone_end=3'	-1	TCCAAGCAAAAGTTATGCAATAAGAC AGAATATAAAGTCTCCGAGAGCCT
5458	db mining	Hs.230485	AI809184	5395750	wh75d08.x1 cDNA, 3' end /clone=IMAGE:2386575 /clone_end=3'	-1	GGGTGGGGTGGGGTGAGAGTGTGTG GAGTAAGGACCTTCAGAAATTAATAT
5459	db mining	Hs.292761	AI809305	5395871	wh75g11.x1 cDNA, 3' end /clone=IMAGE:2386628 /clone_end=3'	-1	TGCAGTTCCTATTTTCTTTTGCCTGTG ATAATTGCAATCCGTCAATAGAA
5460	Table 3A	Hs.210385	AI809310	5395876	wh75h08.x1 cDNA, 3' end /clone=IMAGE:2386623 /clone_end=3'	-1	TGCAAGTTTCTGAGACTGTGAAAAGT GTTTGTCTCTTTGTACCCAAT
5461	db mining	Hs.90463	AI809378	5395944	wa27e12.x1 cDNA, 3' end /clone=IMAGE:2299342 /clone_end=3'	-1	TCCCAGCGAATGTGAATCATTTAGTG TGCTACTCAAATAGGTGTCCAC
5462	Table 3A	Hs.257466	AI809475	5396041	UI-H-BI3-ald-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2736471 /clone_end=3'	-1	TAAGATGTAGGGGCCACCGGCCAGC AGTACCCAGCAATGACCACATATCAG
5463	db mining	Hs.208153	AI809564	5396130	wh76e01.x1 cDNA, 3' end /clone=IMAGE:2386680 /clone_end=3'	-1	ATAAATGAAAGCATACCAAGTGCTGT CCATTCCATAGGTACAACTATGGA
5464	db mining	Hs.310486	AI809746	5396312	7e96g11.x1 cDNA, 3' end /clone=IMAGE:3293060 /clone_end=3'	-1	CTGGTATTCTGAGGTCAGATGTAGGC TGTTGCTCGCTCCGGCTGGGTCTC
5465	Table 3A	Hs.277293	AI811065	5397631	tr03f05.x1 cDNA, 3' end /clone=IMAGE:2217249 /clone_end=3'	-1	CCATCGGGGGTATTGGGGTTTGGG CTGAATTACTTGATTATTGAAAAA
5466	Table 3A	Hs.86693	AI817153	5436320	EST380760 cDNA	-1	GCCAGATTGTGGCAGGTAAAGAGAC AATGTAATTTGCACTCCCTATGATA
5467	Table 3A	Hs.230492	AI818596	5437675	wk74d04.x1 cDNA, 3' end /clone=IMAGE:2421127 /clone_end=3'	-1	TTTAAAGAGGAGGAGGATTTCGGG TTAAACTTTTATTGGCCCCCAT
5468	Table 3A	Hs.229990	AI818777	5437856	wi11f10.x1 cDNA, 3' end /clone=IMAGE:2424619 /clone_end=3'	-1	TAAACCCCAAGACTTCAGATTAGCC GAATTGTGGTGTTCACAGGCCG
5469	Table 3A	NA	AI818951	5438030	wj89e12.x1 NCI_CGAP_Lym12 cDNA clone IMAGE:2410030 3' similar to WP:C11H1.7 CE18492 ;contains Alu r	-1	CTAAGCATGGGGAAGGGGCGAGAGT GAGGACTGTGCCATTGATTAAAGTG
5470	Table 3A	Hs.51039	AI823541	5444212	KIAA0076 gene product (KIAA0076), mRNA /cds=(86,5182)	-1	GTACAGAAACATATTCATGCTTTGA AATAAAGGGAAGTGCTCTCCTGTT
5471	Table 3A	Hs.211535	AI823649	5444320	wi85g03.x1 cDNA, 3' end /clone=IMAGE:2400148 /clone_end=3'	-1	GAAGCCTTTTCTTTCTGTTCAACCTC ACCAAGAGCACAACTTAATAGG
5472	Table 3A	Hs.304477	AI824522	5445193	bx71d03.x1 cDNA, 3' end /clone=IMAGE:2275013 /clone_end=3'	-1	ACCGATCGTTTTAGGATAATATGCA TGTTTCAAGTGGTATTGAAACCCCC
5473	db mining	Hs.270624	AI825096	5445859	7b65e05.x1 cDNA, 3' end /clone=IMAGE:3233120 /clone_end=3'	-1	TGAGGACAGGCTGCCTAAAGTCTAA TTGGAGAGTTAACCTAATGTCTGT
5474	Table 3A	Hs.117906	AI825645	5446316	wb75b09.x1 cDNA, 3' end /clone=IMAGE:2311481 /clone_end=3'	-1	CACCATCGTGGCTCTGAGAACTGAC GCCGTGAATGTTGACCTGAGTGCCG
5475	Table 3A	Hs.229993	AI827451	5448122	wi17d11.x1 cDNA, 3' end /clone=IMAGE:2425173 /clone_end=3'	-1	GGGGAGAGACCACCTAGACATTTG CATTTTGTAGATTAGCCAGCCAAT
5476	Table 3A	Hs.181400	AI827911	5448669	602650370T1 cDNA, 3' end /clone=IMAGE:4761353 /clone_end=3'	-1	TGGATAAATCTGAGCAACTTCTCTCT TGTGCTCCAGGAACCTACGCACT
5477	Table 3A	Hs.342617	AI827950	5448708	ha15h10.x1 cDNA, 3' end /clone=IMAGE:2873827 /clone_end=3'	-1	TGTGGGTTTTGATTGACATACTGTG TTCATGCTGAAGTTTGAGTGCTGT
5478	Table 3A	Hs.132238	AI829569	5450240	wf28e02.x1 cDNA, 3' end /clone=IMAGE:2356922 /clone_end=3'	-1	GGTGTGCACTCCGCTGAAAGCCTT CCCTTTAGCTATTAGGAATTGAGTC
5479	db mining	Hs.289878	AI831819	5452490	wh84f12.x1 cDNA, 3' end /clone=IMAGE:2387471 /clone_end=3'	-1	ACATTGAAAAGAAACCTACAACTGT AATGAATATGAAAAGAATTGTCTAAAA
5480	Table 3A	Hs.341177	AI832038	5452709	wj99e02.x1 cDNA, 3' end /clone=IMAGE:2410970 /clone_end=3'	-1	AAAACCGTTTTCCCATACATAAAGA ACAGGGGTACTCCCGCCCTGATGG

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5481	Table 3A	Hs.210995	AI832182	5452853	td13h11.x1 cDNA, 3' end /clone=IMAGE:2075589 /clone_end=3'	-1	TTTGGTGAAGTGAAAGAGAGAAGTTG CTCTAAAAGGTTGGAACAGCCC
5482	Table 3A	Hs.249031	AI832183	5452854	wh80g09.x1 cDNA, 3' end /clone=IMAGE:2387104 /clone_end=3'	-1	TGGACTGTTGTAATGTTTTGCGTTAT CAAAATGAAAACCTGCCAAATGAGA
5483	Table 3A	Hs.63908	AI858771	5512387	hypothetical protein MGC14726 (MGC14726), mRNA /cds=(21,653)	-1	GCTTTGAGTTTTGGGATGGTCACATG ACACAATCCAGCACTTGAACCTGA
5484	Table 3A	Hs.252259	AI859076	5512692	ribosomal protein S3 (RPS3), mRNA /cds=(22,753)	-1	AGAGCCATTCCACAAAGTAAATGTG CAGTGCCCATGTTTCTTGTTTA
5485	Table 3A	NA	AI860120	5513736	wh39e01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2383128 3', mRNA sequence	-1	GACTCTGAGAGAGAGCGACGGCCAT CATAGAACAGCGAAGGAGTCGATC
5486	db mining	Hs.156811	AI862332	5526439	hz33g10.x1 cDNA, 3' end /clone=IMAGE:3209826 /clone_end=3'	-1	ATCGATGAGAAGAGTCTGCAAAACAC TTCATCCTCAGGACGTGCTGTCT
5487	db mining	Hs.304508	AI862595	5526702	wh99g01.x1 cDNA, 3' end /clone=IMAGE:2388912 /clone_end=3'	-1	ATATATTAACACAGGTATTAGAGA CATGAATTGCACCCAAACACAGCT
5488	Table 3A	NA	AI862623	5526730	wh99h10.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2388931 3', mRNA sequence	-1	ATTCATTCGGGTCTTCTTTCTCCG CCCCCTCCTCCATTGGCACCTC
5489	Table 3A	Hs.181426	AI865427	5529523	EST367815 cDNA	-1	TCAGTTTTGTGGAATCTGGTGTTCG ACTATAGGTTAAGAGTTGCCATT
5490	Table 3A	Hs.341208	AI865603	5529710	wk47g03.x1 cDNA, 3' end /clone=IMAGE:2418580 /clone_end=3'	-1	TGTGTGGTGGGGTGCCTTTGAGGTT GGAGGAAAGTAGACAGCGAAAC
5491	Table 3A	Hs.9788	AI866194	5530301	hypothetical protein MGC10924 similar to Nedda4 WW-binding protein 5 (MGC10924), mRNA /cds=(104,769)	-1	TGTGCTTTTTGCCAAGTGGAATTC ATCTTGTTTGCTATGTTAAACT
5492	Table 3A	Hs.224760	AI874107	5548156	wm49b01.x1 cDNA, 3' end /clone=IMAGE:2439241 /clone_end=3'	-1	CTTTGGGGACCTAAACCCAGGTGG TCTCTTGTTGTTAATAATGCTGGAA
5493	Table 3A	NA	AI880542	5554591	al80h05.x1 Barstead colon HPLRB7 cDNA clone IMAGE:2378361 3' similar to SW:ATP6_HUMAN P00846 ATP SY	-1	AAATCGCGGTGCGCTTAATCCAAGCC TAGGTTTTACACTTTTAGTAAGC
5494	Table 3A	Hs.220850	AI880607	5554658	ym91d11.r1 cDNA, 5' end /clone=IMAGE:166293 /clone_end=5'	-1	TGGGGCACTTTGAAAACCTTACAGGC CCACTGCTGCTTGCTGAAATAAAA
5495	Table 3A	Hs.89414	AI884548	5589712	chemokine (C-X-C motif), receptor 4 (fusin) (CXCR4), mRNA /cds=(88,1146)	-1	GACATTCATCTGTTTCCACTGAGTCT GAGTCTCAAGTTTCACTCCAGC
5496	Table 3A	Hs.23096	AI884671	5589835	602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5'	-1	TGGCGAGGATAAATAGAGGCATTGTT TTTGCTACTTTGCATATCATTGGC
5497	db mining	Hs.34650	AI885574	5590738	602286784T1 cDNA, 3' end /clone=IMAGE:4375724 /clone_end=3'	-1	TGGCTCTCCTCTTTGTAATATACAGG GTGAACCTCTTACTGATACACACA
5498	Table 3A	Hs.121572	AI886313	5591477	EST387650 cDNA	-1	CCAGTGCTCTGCATGGGTGCTAGGC TGAATTATTTGTAATTGTGCTTAGG
5499	Table 3A	Hs.213385	AI912585	5632440	we11d07.x1 cDNA, 3' end /clone=IMAGE:2340781 /clone_end=3'	-1	ACCGTCTTTTGTGATTCCCTGGAAAC CCTTAATTCAATAGTCCTGACTGA
5500	Table 3A	Hs.228488	AI917348	5637203	ts83d10.x1 cDNA, 3' end /clone=IMAGE:2237875 /clone_end=3'	-1	AGCCCTGGGTAGCCAAGTGATTTTCC CATTCCCAAAGTTAGTAAACCTTT
5501	Table 3A	Hs.179391	AI917642	5637497	wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3'	-1	GCAGGAAAGATGGGGTGGTGGACTG TTTTTGCTACTTTTGTTTTGAA
5502	Table 3A	Hs.337286	AI922889	5658853	wn64g11.x1 cDNA, 3' end /clone=IMAGE:2450276 /clone_end=3'	-1	CCCCCTGAAACTGGCATTTTGTAAT GTGGTTTGACTATTTTGTATGTT
5503	Table 3A	Hs.212553	AI922921	5658885	wn81c05.x1 cDNA, 3' end /clone=IMAGE:2452232 /clone_end=3'	-1	ACCTGAGAAATTCCTAAGGCCAAAG CAAGGTAACAGGGACTTCAGTTTT
5504	Table 3A	Hs.58643	AI926251	5662139	602438603F1 cDNA, 5' end /clone=IMAGE:4564968 /clone_end=5'	-1	GCCTCAGTACAAAGGGGGCTTTGGA AGTGTGTTGTGGCTGAATAAGGAA
5505	Table 3A	Hs.40328	AI927454	5663418	nab63b04.x1 cDNA, 3' end /clone=IMAGE:3272383 /clone_end=3'	-1	ACCATGCCAATTGAAGAACGTGTTA AAGATGAGGAGGAGAGATGTACCA
5506	db mining	Hs.154366	AI934956	5673826	ng40b06.s1 cDNA, 3' end /clone=IMAGE:937235 /clone_end=3'	-1	GCACATTCCTTCTTATATCTTGAA GCACCCAGATATCTTCATGTCCC
5507	Table 3A	Hs.101370	AI936516	5675386	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	TTAAGTCATCTGCTGACGAGTGTCT GTGTCAACCTCCTCCTAGGTAACC
5508	Table 3A	Hs.180448	AI948513	5740823	Importin beta subunit mRNA, complete cds /cds=(337,2967)	-1	CAGGGTATCAGATATTGTGCTTTTG GTGCCAGGTTCAAAGTCAAGTGCC
5509	Table 3A	Hs.71245	AI954499	5746809	zl17f11.r1 cDNA, 5' end /clone=IMAGE:502221 /clone_end=5'	-1	TGGTAATAGTGTGTTGACTCCAGGGAA GAACAGATGGGTGCCAGAGTGAAA

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5510	Table 3A	Hs.118820	AI955314	5747624	Homo sapiens, clone IMAGE:3357862, mRNA, partial cds /cds=(0,325)	-1	TCAAGTATACCATTTAAAAATTTTCAT CAGGCAGAGCCCTGACCAGGAAA
5511	db mining	NA	AI961962	5754664	wt40g09.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2509984 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION	-1	CTTTTCCGGTTGCCCGAGGATGCTTG GGAAGGAACCCGCTCTCCCTTCTTC
5512	Table 3A	Hs.341528	AI962127	5754840	wx77f07.x1 cDNA, 3' end /clone=IMAGE:2549701 /clone_end=3'	-1	TCCCCAAACCCCTTAAAGGTTTTTA AATTGTTTCAAATCTGGGCAAGTT
5513	Table 3A	Hs.37121	AI968387	5765205	phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3), mRNA /cds=(0,3704)	-1	GACTCGGAGAGCCAGGAGGAGAACA CGCAGCTCTGAACTGGCTGAGCGAG
5514	db mining	Hs.13034	AI969716	5766534	hv63f09.x1 cDNA, 3' end /clone=IMAGE:3178121 /clone_end=3'	-1	CTGTTGTGAATCATTTGTGTCCTTTTC AACTGTCTTTCAGAGGAAAGGTA
5515	Table 3A	Hs.193247	AI978581	5803611	hypothetical protein DKFZp434A171 (DKFZp434A171), mRNA /cds=(113,2584)	-1	AAGAAGCAACCACAGCTAATTTTAGA ACATGCACTCTGACAGAAAAGACA
5516	Table 3A	Hs.153	AI984074	5811293	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	-1	GCTTTTGAGGACCTTTCTGGAGGAAA GGAAAAGCCGTGTTTGGGGAGTCT
5517	Table 3A	Hs.7557	AL042081	5421426	FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526)	-1	AGGCTGCATATGGATTGCCAAGTCAG CATATGAGGAATTAAGACATTGT
5518	Table 3A	Hs.133262	AL044498	5432716	DKFZp434I082_s1 cDNA, 3' end /clone=DKFZp434I082 /clone_end=3'	-1	AAGACTAGAGCTACACTAGGCCACTA TCTTATTACACGACAGCACAAACAT
5519	Table 3A	Hs.39911	AL138429	6855110	mRNA for FLJ00089 protein, partial cds /cds=(62,1111)	-1	TTAAGAACCCCAAAGATTAAAGGAAA CAATGTTAAGGGCTTTTGTGAGGA
5520	Table 3A	Hs.89986	AL515381	12778874	cDNA /clone=CL0BB017ZH06-(3-prime)	-1	CGGAAAGTCGAAATCAAATCTATGCTT TTAATTGAAACCGTGCCTGAAACG
5521	Table 3A	Hs.9096	AL520535	12784028	hypothetical protein FLJ20473 (FLJ20473), mRNA /cds=(57,1472)	-1	TCTTCACCAAGTTCAAGCTCCGTGGG CCCACTGCTGCTGTGCCAAGAG
5522	Table 3A	Hs.13144	AL521097	12784590	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	-1	GATACACTGTCCAGCCAGGTCAG GCCCTAGGTTCTTTACTCTAGTAC
5523	Table 3A	Hs.118142	AL522477	12785970	AL522477 cDNA /clone=CS0DB008YK14-(3-prime)	-1	TGGAATTTACTAAATTTGAAATTAAC GTAACCGAAGCAACAACCGGCAA
5524	Table 3A	Hs.295112	AL528020	12791513	KIAA0618 gene product (KIAA0618), mRNA /cds=(1041,4040)	-1	GCGGGAGGCTGGGACTTTCCATTAC AAATAGAGACTCAATCTCTGTGAG
5525	Table 3A	Hs.26670	AL540260	12870241	AL540260 cDNA /clone=CS0DF032YF03-(3-prime)	-1	ACTCAGGTGGTGTGGTGTAGTGAT GCTGGAGAAGAGAATATTACTGGT
5526	Table 3A	Hs.285013	AL543900	12876379	putative HLA class II associated protein I (PHAP1), mRNA /cds=(148,897)	-1	CAGGTTGCTTTCGTGTCCTCTTCTGT GTTGCTTTAGAAGTGACGTGTAAT
5527	Table 3A	Hs.183232	AL561892	12909772	hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476)	-1	AAACACAGCCACCCCATTTTCAGACC GCCTTCCTGAGGAGAAAATGACAG
5528	Table 3A	Hs.21812	AL562895	12911771	AL562895 cDNA /clone=CS0DC021YO20-(3-prime)	-1	GCTAACTGGATAAAGTTTGTGCAGAC ATTCTGAGTGTCGATATTGACC
5529	Table 3A	Hs.21812	AL562895	12911771	AL562895 cDNA /clone=CS0DC021YO20-(3-prime)	-1	GCTAACTGGATAAAGTTTGTGCAGAC ATTCTGAGTGTCGATATTGACC
5530	Table 3A	Hs.181165	AL565736	12917408	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441)	-1	AGCTGGCTTCACTGCTCAGGTGATTA TCCTGAACCAACAGGCCAAATAAG
5531	Table 3A	Hs.77393	AL567986	12921892	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDP5), mRNA /cds=(114,1373)	-1	AGTCAGGACTGTCTAGGTCAGGGAA GCCAAGATGTCTGAAGAGAGAGGAA
5532	Table 3A	Hs.13256	AL570416	12926702	AL570416 cDNA /clone=CS0DI020YK05-(3-prime)	-1	ATTCAACCAGTAATGGTACCTGAGGA ATTGAAATGGGTATTGTTTCTGT
5533	Table 3A	Hs.180546	AL571386	12928631	AL571386 cDNA /clone=CS0DI009YL09-(3-prime)	-1	AGTGGAGAGGCCCTGTTAGTTTACTT TTCATATTGAGTGATGCATGAGGT
5534	Table 3A	Hs.21732	AL573787	12933363	AL573787 cDNA /clone=CS0DI055YM17-(3-prime)	-1	GCATTCTATTTAAAAAGGGAGTGGGG AGCAAATGAAAATTAAATGTGGGG
5535	Table 3A	Hs.23294	AL574514	12934790	hypothetical protein FLJ14393 (FLJ14393), mRNA /cds=(60,1454)	-1	TCACCAGGAAAACATGCTTGTGAATT GTGCAGTAAAGGTTGCTGAATGACT
5536	Table 3A	Hs.181392	AL575666	12937052	major histocompatibility complex, class I, E (HLA-E), mRNA /cds=(7,1083)	-1	CCTTTTCTCTCCCATGACCTTTAACA GCATCTGCTTCATTCCCCTCACC
5537	Table 3A	Hs.85258	AL575755	12937231	CD8 antigen, alpha polypeptide (p32) (CD8A), mRNA /cds=(65,772)	-1	CTGAGAGCCCAACTGCTGTCCCAAA CATGCACCTCCTTGCTTAAGGTAT
5538	Table 3A	Hs.169810	AL576149	12938006	mRNA for transmembrane glycoprotein (CD44 gene) /cds=(178,2406)	-1	TGAGTGAAAGCAAGCTGTGAAACATTC TGCGTTTATGCAACTTCCTTGCCT
5539	Table 3A	Hs.174905	AL577970	12941605	mRNA for KIAA0033 gene, partial cds /cds=(0,1008)	-1	CAAGAAGACAAGCATCTGTGGTGGC GAGGCAAGCAGGCTAACTAGGAGTT
5540	Table 3A	Hs.5057	AL578975	12943566	AL578975 cDNA /clone=CS0DK012YN01-(3-prime)	-1	TGCGCCCAAGTGATTGATTGCTTTA TCTTTGGTACTTTTACTGTAATGG
5541	Table 3A	Hs.278555	AL582047	12949649	AL582047 cDNA /clone=CS0DL003YD01-(3-prime)	-1	CATCCAGCACTAATTTTCATGCATTTA TGAAAGGATGCGCAGGACCCCT
5542	Table 3A	Hs.198296	AL582354	12950255	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015)	-1	AGCCTGAGGCAAAATAAATTCAGTA ATTTGGAAGAAATGGGTGTTGGCAA

Table 8

5543	Table 3A	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTTGAGATG GAATGTAGGCCCTGATGTTATGCT
5544	Table 3A	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTTGAGATG GAATGTAGGCCCTGATGTTATGCT
5545	Table 3A	Hs.7187	AU158636	11020157	mRNA for KIAA1757 protein, partial cds=(347,4576)	-1	AGTGGAGTGTTTACACCTTGCTGTAA CATTGAACCTTTCACAAGAGATGT
5546	Table 3A	Hs.86671	AV648638	9869652	602079785F2 cDNA, 5' end /clone=IMAGE:4254068 /clone_end=5'	-1	ATATCATATTATTGATGCCATTAGGC GGCCTGGATCACCATTCTAAGT
5547	Table 3A	Hs.343475	AV648670	9869684	601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3'	-1	GCCACCAGACAGAAGGACCAGAGTT TCTGATTATAACAATGATGCTGGG
5548	Table 3A	Hs.2730	AV650434	9871448	heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704)	-1	TGTTGGTGAGCAATGTGCAGAGGCCA GAGCCGCTGAAGTATGGTTCCTGAG
5549	Table 3A	Hs.312582	AV651615	9872629	601439711F1 cDNA, 5' end /clone=IMAGE:3924482 /clone_end=5'	-1	GGCTGCTGTTGACTGAAATTCCTATC CTCAAAATACTCTAGACTGAAGCT
5550	Table 3A	Hs.5897	AV653169	9874183	cDNA FLJ13388 fis, clone PLACE1001168 /cds=UNKNOWN	-1	CTTTTTAGTAGGCAAAGGTTCTTCTTC CTCCTCTTTTGGTGACGGGACGC
5551	Table 3A	NA	AV654188	9875202	AV654188 GLC cDNA clone GLC DTC01 3', mRNA sequence	-1	GCGTGTATGTGGGATGCCATAGGTG TGACTGTAGAGTCATTCTTCTTCC
5552	Table 3A	Hs.38218	AV659358	9880372	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	TGTAAGTTGACTTTCAAAAGTCTCTG GAAACACTGGACTTAGCTGTGTC
5553	Table 3A	Hs.133333	AV661783	9882797	AV661783 cDNA, 3' end /clone=GLCGXE12 /clone_end=3'	-1	GAAGCGTGGCAGAGAATATGGATC AGGCAGCCCCTCTCATCTTACCAT
5554	Table 3A	Hs.85844	AV700210	10302181	neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA /cds=(0,2390)	-1	TTGGTCCAAACTCTGGAGCCTTGCG GAGAACATAGGCGCAATAAGTGTT
5555	Table 3A	Hs.285173	AV700298	10302269	602632207F1 cDNA, 5' end /clone=IMAGE:4777537 /clone_end=5'	-1	CCCTTCTTAGTAAAGAGACATCTTCT ACAGTAACCACAGAGAAGAGTGG
5556	Table 3A	Hs.238730	AV700542	10302513	hypothetical protein MGC10823 (MGC10823), mRNA /cds=(63,1235)	-1	TGGACATAACCTGGGTGAGAAGAGAA ACTTTTGAAGCTACACGAACAAGC
5557	Table 3A	Hs.284674	AV700636	10302807	AV700636 cDNA, 3' end /clone=GKBAGH12 /clone_end=3'	-1	CGGCTCAAATAAACCTTTACCGGATT TTTGGGGTTATGCCACACCCCTTG
5558	Table 3A	Hs.240077	AW002624	5849540	wu60d10.x1 cDNA, 3' end /clone=IMAGE:2524435 /clone_end=3'	-1	GGACCACTAGTACTTCCAGAACCATAA TATAACTAGACATGCCTGGAATGC
5559	Table 3A	Hs.301704	AW002985	5849991	eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2080)	-1	AACAAGCCATGTTTGCCCTAGTCCAG GATTGCCTCACTTGAGACTTGCTA
5560	Table 3A	NA	AW004905	5853768	wz82d03.x1 NCI_GCAP_Gas4 cDNA clone IMAGE:2565317 3' similar to SW:ATP6_HUMAN P00846 ATP SYNTHASE A	-1	TCTACTGACTATCCTAGAAATCGCTG TCGCCTTAATCCAAGCCTACGTTT
5561	Table 3A	Hs.173280	AW005376	5854154	ws94a12.x1 cDNA, 3' end /clone=IMAGE:2505598 /clone_end=3'	-1	GAGAAACTCCGTGCATGAAGGTTTC CTCCTTGACTCGGCAGCAGCGGCC
5562	Table 3A	Hs.233560	AW006045	5854823	wz81b09.x1 cDNA, 3' end /clone=IMAGE:2565209 /clone_end=3'	-1	CCAAGTAGGTTTTAACTCTGGTATGG TCTCGTGTTCATTGTGTGCA
5563	Table 3A	Hs.159643	AW006352	5855130	wt04d12.x1 cDNA, 3' end /clone=IMAGE:2506487 /clone_end=3'	-1	GTTCCCACGGAGCTGACTTCTCCGG GGTGCCGTGTGCCCTACATTAACCC
5564	Table 3A	Hs.231987	AW006867	5855645	602320903F1 cDNA, 5' end /clone=IMAGE:4424065 /clone_end=5'	-1	CCGTAACCTCCGACAAACGAGAACTT CTTGAGGCTTTCTTCTTAAGGA
5565	db mining	Hs.157118	AW009081	5857859	ws76g10.x1 cDNA, 3' end /clone=IMAGE:2503938 /clone_end=3'	-1	TCTGGACCCTGCTTGGGTTACAGCA TTGGTGGAGGTAAGTAGTATTCTC
5566	Table 3A	Hs.134272	AW009671	5858449	ws85g09.x1 cDNA, 3' end /clone=IMAGE:2504800 /clone_end=3'	-1	GAAGAGGAAGCTCATCCGAAGTCTTC CGACAGAGTGAGCCGTATGCCCCG
5567	db mining	Hs.131887	AW009730	5858508	602415255F1 cDNA, 5' end /clone=IMAGE:4523725 /clone_end=5'	-1	AGTGTGTATTCTTGATGTTTATTGGCT CATGTGGACAGAAATGTACAGGG
5568	Table 3A	Hs.232000	AW016002	5864759	UI-H-B10p-abh-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	AGATGAGGCTGCTCTGAAGATTCACT AATTAGGATGGACAGTCAGCTACT
5569	Table 3A	Hs.233261	AW026667	5880120	wv15d09.x1 cDNA, 3' end /clone=IMAGE:2529617 /clone_end=3'	-1	TGGGCTTTGGGGTTTCAAGTTGTTACC TTTGGAGACTTATTTAATGAACC
5570	Table 3A	Hs.101340	AW026713	5880166	EST380762 cDNA	-1	CAGTGGTTCTGAGAGAATCTTAGTT CAAAGGACTGCCCCGCCAACCC
5571	Table 3A	NA	AW027160	5885916	wt72b08.x1 Soares_thymus_NHFTth cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive element	-1	ACGCCAAAGCCAAATCATCCACTTTC AGTACTTACCTAACCAATCTCCCA

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5572	Table 3A	Hs.233564	AW027530	5886286	wv74c06.x1 cDNA, 3' end /clone=IMAGE:2535274 /clone_end=3'	-1	CAGGATGTTATTGACAGGGTGGCCTT TGTGATTCCCTCCGGTGGTGGCAGC
5573	Table 3A	Hs.311783	AW043857	5904386	wy81g04.x1 cDNA, 3' end /clone=IMAGE:2554998 /clone_end=3'	-1	GCCATTTTCATTGTGTGTGGTTAGA CTTCCAGGAGGCTGTTTAGCTCTA
5574	Table 3A	Hs.277672	AW050975	5913245	wz25f04.x1 cDNA, 3' end /clone=IMAGE:2559103 /clone_end=3'	-1	CCTTTGTGAAAAGTCACCTGTGACTG TCAGGGGTATGCTATGGGCCCTTTT
5575	db mining	Hs.279066	AW063114	8887051	TN0103 cDNA, 3' end /clone_end=3'	-1	GATCCACTTTGGGGTTCGGCGGCAG ATTATTCGGCTGGTAGAGCGGATG
5576	db mining	Hs.279082	AW063120	8887169	TN0257 cDNA, 3' end /clone_end=3'	-1	AATAAGGGAAGTTCATTATGACAGC AAATGTTGTTTGTATTGGCTTGC
5577	db mining	Hs.279083	AW063153	8887202	TN0786 cDNA, 3' end /clone_end=3'	-1	CTTCATGGTCTCCAGCCAGGACTCCA TCAGCGCCACGGCTTCATCCGAAC
5578	db mining	Hs.279127	AW063155	8887204	DP1003 cDNA, 3' end /clone_end=3'	-1	TTGATGCTCATCTGCTCGAGGTG ATTGATGCCAGGTGACGCACCAT
5579	db mining	Hs.279104	AW063156	8887205	TN0974 cDNA, 3' end /clone_end=3'	-1	TCCTTTGGATAAGGTCCAAAACTGT AACACATGACCCTCAGAGCCCTTT
5580	db mining	Hs.279085	AW063158	8887207	TN0311 cDNA, 3' end /clone_end=3'	-1	CCCGGCGACTTCACCAACCCGCTATCT GGGCACCAAGACTATATCTAGAT
5581	db mining	Hs.279086	AW063159	8887208	TN0312 cDNA, 3' end /clone_end=3'	-1	CGCAATAGTCTCGACAAGTCGCCAA CCCTCCCACTTCGGTCCGATCAGCT
5582	db mining	Hs.279092	AW063191	8887240	TN0359 cDNA, 3' end /clone_end=3'	-1	CGTCGGGTACCTCGCCGATAAAATC GCTGATGGCCTGGTCCGATCCTGAAG
5583	db mining	Hs.279093	AW063196	8887245	TN0360 cDNA, 3' end /clone_end=3'	-1	ATCTTATCCCTCTGTACTCAATGTGA GTGCATACTTTACATTGGCTACT
5584	db mining	Hs.279102	AW063210	8887259	TN0377 cDNA, 3' end /clone_end=3'	-1	GGTCCTTGAAGATGACGCGGATGAT CGAGGTCTCTGCGCGGTAGGCCGATG
5585	db mining	Hs.279067	AW063230	8887055	TN0107 cDNA, 3' end /clone_end=3'	-1	ATGATGAAGCTGCTGTCCAACGCCTT CGTCTGCCAGTTCTGCTGGTGTG
5586	db mining	Hs.279069	AW063239	8887064	TN0018 cDNA, 3' end /clone_end=3'	-1	TCCTTGCCAGAGCCTTCGGGTTCTAC GATTTGATCGACGACGCTGGTGTG
5587	db mining	Hs.279070	AW063242	8887067	TN0138 cDNA, 3' end /clone_end=3'	-1	TCGAACATGGGCAGCTCCGTTTCAAG ATGGCTCAAGACTAGCGGATTGGG
5588	db mining	Hs.279071	AW063246	8887071	TN0358 cDNA, 3' end /clone_end=3'	-1	AGTGATAGAGACCAAGACTGCTTTT TAATTTTGTGGGGAGGGGGTGGGA
5589	db mining	Hs.279072	AW063252	8887077	TN0149 cDNA, 3' end /clone_end=3'	-1	CGGGTCACTCATGTTGGCTACTAAC CTTTTCGTGCGCCGGGCATTCTAG
5590	db mining	Hs.279087	AW063267	8887092	TN0331 cDNA, 3' end /clone_end=3'	-1	CTTGCTCCTGATCGCTTCTTCTCTG CAAGGGAGAGCTTCTGGACCTTCA
5591	db mining	Hs.279073	AW063271	8887096	TN0156 cDNA, 3' end /clone_end=3'	-1	CTTGTTTGACATCAGCGCCATCTCGA CAGCGTATTCGCTATGACTGTTT
5592	db mining	Hs.279074	AW063274	8887099	TN0792 cDNA, 3' end /clone_end=3'	-1	CACGAAGCCTTCGATCAGTTGCAGCA CGCGGCCAGAGCGGTGATAGAAC
5593	db mining	Hs.279122	AW063299	8887124	TN0185 cDNA, 3' end /clone_end=3'	-1	CATTTTGCCATCTGCGAGCATCTGGG TATTGACATGATCCCCAGTGAGC
5594	db mining	Hs.279076	AW063319	8887144	TN0230 cDNA, 3' end /clone_end=3'	-1	CACCAAGCTGGTCAACATCCAGGCG AATGGCTATTACGTGGATGAGATCA
5595	db mining	Hs.279078	AW063325	8887150	TN0236 cDNA, 3' end /clone_end=3'	-1	TTGCTGATACGGCCTTTGATCATGTT TTCAACGATGTTTTCCGGCTTGCC
5596	db mining	Hs.279079	AW063327	8887152	TN0238 cDNA, 3' end /clone_end=3'	-1	CCTCGACAACTAAATGTTGATTGA ATTGGCCTGTTATCATCTTGATCAC
5597	db mining	Hs.302423	AW063352	8887289	TN0725 cDNA, 3' end /clone_end=3'	-1	GTTTCAGATCGGGCCGCTCCGCCCG GGTACCTATAGCGGAATCGAATTT
5598	db mining	Hs.279095	AW063358	8887295	TN0979 cDNA, 3' end /clone_end=3'	-1	GAAAAACAGAAATGATGCTCGGCACAT TCTCGTCCAGCACCTCGGCACCGG
5599	db mining	Hs.279096	AW063371	8887308	TN0746 cDNA, 3' end /clone_end=3'	-1	AACTGTATTGATCAGCTGGCGCTG ATGGTGTGACGAGTCGCTTGTTC
5600	db mining	Hs.279097	AW063372	8887309	TN1085 cDNA, 3' end /clone_end=3'	-1	AGTTGACATATAACCCACTTTACATAC ATTCCAAAATTGCGAGTAGTGAGT
5601	db mining	Hs.279075	AW063428	8887365	TN0121 cDNA, 3' end /clone_end=3'	-1	ATATCGTACCGAGAACTAGTGCGGA TATCTGACCAGGTATGGCGGTTGG
5602	db mining	Hs.279099	AW063436	8887373	TN0922 cDNA, 3' end /clone_end=3'	-1	GTGGATGACCTGATCCAGGTGCGCC TGATCGGCCTGACTGATGAGCTGTC
5603	db mining	Hs.279100	AW063458	8887395	TN0949 cDNA, 3' end /clone_end=3'	-1	ATGATGACCAGATGCTCTGGCACCGT GTCGAGTTCGAGGATGCCGACATT
5604	db mining	Hs.279103	AW063469	8887406	TN0981 cDNA, 3' end /clone_end=3'	-1	GATCTGGGACGCATGGCCGAAGCTG AAAAGCTGGCTGTAGAAGACCTCGA
5605	db mining	Hs.279101	AW063474	8887411	TN0354 cDNA, 3' end /clone_end=3'	-1	AACATGGCAATATTTATTGGTCTAAT ACTGTCCTGGCAAGGTTGGTGT
5606	db mining	Hs.279821	AW063497	8887434	TN0113 cDNA, 3' end /clone_end=3'	-1	GAGGCAGAGGTGTAGCGAGTCCAGG CTCTCTCGAACGTTGCACCCGACG
5607	db mining	Hs.279105	AW063509	8887446	TN1012 cDNA, 3' end /clone_end=3'	-1	GTCCACACGTTCCGGCCCTGACTCT GCTGTGTTGACGAGGACAATCTCG
5608	db mining	Hs.279089	AW063534	8887471	TN1054 cDNA, 3' end /clone_end=3'	-1	CATGACGTTGTGCTCGACACCCCAAC AGATCACGTAATCAGCCTGGTGGA
5609	db mining	Hs.279080	AW063546	8887483	TN0243 cDNA, 3' end /clone_end=3'	-1	TAGGCTATAGAGATGTGAGGGATTAT TATTAGTCACACCTCTAGTCATGCC
5610	db mining	Hs.279108	AW063552	8887489	TN1055 cDNA, 3' end /clone_end=3'	-1	GGCTGCCGGATGTGTAGTCTTCCC ATGTTGTGAAGTAACGGTGTCCAC

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5611	db mining	Hs.279109	AW083556	8887493	TN1059 cDNA, 3' end /clone_end=3'	-1	TGCCCTGTATAGTGTGTAATAAATTA GAATGTTTACCCCAAAACCATCTGG
5612	db mining	Hs.279110	AW063561	8887498	TN1066 cDNA, 3' end /clone_end=3'	-1	GTCTTTTGAATCGCTCTTTAGCTCGT GCGGGGCTGTTGTCCCACTTGTG
5613	db mining	Hs.279090	AW063572	8887509	TN1079 cDNA, 3' end /clone_end=3'	-1	CTATGCGCTGCGCTACAAGCTGGAC CTGTATTCCGACTTCAGCTACTACC
5614	db mining	Hs.279111	AW063598	8887535	DP0133 cDNA, 3' end /clone_end=3'	-1	TTGGAAGCGACGCTGCGTGGCTGCG TCGTCCAATTGCAGCATGGATAAGG
5615	db mining	Hs.302424	AW063600	8887537	DP0925 cDNA, 3' end /clone_end=3'	-1	CCTTCCGCTGTCCCTTCAGTAGCTGT TTCTGTTCCCTGACGCCCACTTCT
5616	db mining	Hs.279124	AW063609	8887546	DP0922 cDNA, 3' end /clone_end=3'	-1	CAATGCAGCGGCTGATGCAGATCAC CCACGAGATGCAGGACGAAGGCGAG
5617	db mining	Hs.279113	AW063630	8887567	DP0154 cDNA, 3' end /clone_end=3'	-1	TCATTAGTCTGAGTAGGAGGAAAGA GGACAGGTTGTTGGAGAGTTGGTT
5618	db mining	Hs.279114	AW063635	8887572	DP0774 cDNA, 3' end /clone_end=3'	-1	TAATTGCCGCTGAAGCACGAATCCTC GAAATGCGTCACTTCGGATTGAC
5619	db mining	Hs.279125	AW063652	8887589	DP0189 cDNA, 3' end /clone_end=3'	-1	AAATGTGGTGACAAAGTACCAGCAAG AACTGGACTGTGTTCTGGAGCCT
5620	db mining	Hs.279116	AW063678	8887615	DP0229 cDNA, 3' end /clone_end=3'	-1	GTTTCATCGTCTCGCTCGCAAGAAGT AAGGGCTAGGCCATGACTCGTTCTG
5621	db mining	Hs.279117	AW063709	8887646	DP0336 cDNA, 3' end /clone_end=3'	-1	CTCTTGGCAGCCCTGCTCTCGTGGG TCAGCATCGTCCGCTGCTCCGTTGG
5622	db mining	Hs.279118	AW063718	8887655	DP0314 cDNA, 3' end /clone_end=3'	-1	GTGCTCGCTGAGCTGGTCCAGAAAT CCGTCGACTGAGGCGATGGCGGCTG
5623	db mining	Hs.279119	AW063746	8887683	DP0347 cDNA, 3' end /clone_end=3'	-1	CATGAACAAGGGCGGATCATCTCTG ATGCCCAACACACTGGACTTCGGTG
5624	db mining	Hs.279120	AW063778	8887715	DP0954 cDNA, 3' end /clone_end=3'	-1	CACCGGTTGTAGGCGACGAGCGTGA ACGAAAACGTGTCCGACGCTTGTGA
5625	db mining	Hs.279121	AW063780	8887717	DP0388 cDNA, 3' end /clone_end=3'	-1	CATATGCGGCTGTGCCATAGCCGGA TGTTCTTCGTGCGTGCCTACCCCG
5626	db mining	Hs.279123	AW063833	8887770	DP0756 cDNA, 3' end /clone_end=3'	-1	TTCTTTCGTCGCGCATCGGAATGCG AAACTCGTACTTCGTGTAGAATCTC
5627	db mining	Hs.279138	AW063909	8887846	SP0953 cDNA, 3' end /clone_end=3'	-1	GCCAGGGGCTTTATCACTTCCATGGC CGCAGCGATGACCAAGTCAAGCTG
5628	db mining	Hs.279126	AW063951	8887888	DP0986 cDNA, 3' end /clone_end=3'	-1	CGCCGACCAAGCTTACCAGCTTCTCG CCGATCTACTGCGACGAGAAAGGC
5629	db mining	Hs.279174	AW063977	8887914	DP1019 cDNA, 3' end /clone_end=3'	-1	GGTAGTGACGTGCTGAATGACGGTG CCGTCCATCATCGGGTGGAGTAAG
5630	db mining	Hs.279128	AW064020	8887957	DP1073 cDNA, 3' end /clone_end=3'	-1	TTCAGGACTCGTTTACAGTAGGCAAC GCTGTCTAAAGTTCCCAAGGATT
5631	db mining	Hs.279130	AW064046	8887983	SP0153 cDNA, 3' end /clone_end=3'	-1	CTCTTTACCCGGAACAGGTTGGGGA GATGACACGACAGAAATCATACGC
5632	db mining	Hs.279084	AW064052	8887989	SP0159 cDNA, 3' end /clone_end=3'	-1	CTTTGGATATATCGAGAAAGGCCAGG GCCTGAACAAGGAAAGCTTCCAGG
5633	db mining	Hs.279825	AW064053	8887990	SP0992 cDNA, 3' end /clone_end=3'	-1	AAGGCTGGTCAAGAATCTTGAGACG GAATTGCACAGTCTCGGCGTATCC
5634	db mining	Hs.279131	AW064080	8887997	SP0636 cDNA, 3' end /clone_end=3'	-1	GATCGATTGCGGGGTGACATCGGCG CTGAGCACCATACCCGGAACATAAG
5635	db mining	Hs.279135	AW064084	8888021	SP0612 cDNA, 3' end /clone_end=3'	-1	CTGAGATCACCTGGAACACCGACAAG GACGAGATCGCAGTCTGCAACCTG
5636	db mining	Hs.279138	AW064098	8888035	SP0575 cDNA, 3' end /clone_end=3'	-1	CTGAAGGCTTTGGCGACACCAAGGT CTATCCGTTTGAATTTGCCGAAAC
5637	db mining	Hs.302426	AW064100	8888037	SP0684 cDNA, 3' end /clone_end=3'	-1	TCTTGTGCCAGCAGCTTGTCTGATA GCCGATGAATCGCGTCCCTTTGTC
5638	db mining	Hs.279175	AW064121	8888058	SP0554 cDNA, 3' end /clone_end=3'	-1	GAATCTCTCAAGGAAATAGTCCACCG CCTGCTGCTTGGACGCTGCCAGTT
5639	db mining	Hs.279139	AW064129	8888066	SP0696 cDNA, 3' end /clone_end=3'	-1	GTGACCTCGGGTCCCGCTTGGTGA GGGTGCCGGTCTTGTGGAAGACGAC
5640	db mining	Hs.279140	AW064136	8888073	SP0570 cDNA, 3' end /clone_end=3'	-1	GTGTTGCGGCTTCATGTGCCAACAC CATCGGCACTGGCATCATCGATCC
5641	db mining	Hs.279108	AW064157	8888094	TN1014 cDNA, 3' end /clone_end=3'	-1	AGGTTGATTCCACTTCCTCGGGAGG TTTCGCCACCTCTTCGCCTTTGAG
5642	db mining	Hs.279141	AW064160	8888097	SP0594 cDNA, 3' end /clone_end=3'	-1	GTTAGCTTCCACGCTTTATCTCCTGC TCTGAGTGTGTACCCGCGCTGCTC
5643	db mining	Hs.279142	AW064161	8888098	SP0595 cDNA, 3' end /clone_end=3'	-1	TTAAAGTGGTAAGGGAGGTTTCTACT CCTGGGGAACATTAAAGTACCTT
5644	db mining	Hs.279143	AW064168	8888103	SP0605 cDNA, 3' end /clone_end=3'	-1	CTTTCTCCGACTTCGAGATCTGCCCG TGGTCGAGATCGTGGTAGATGATG
5645	db mining	Hs.279144	AW064175	8888112	SP0615 cDNA, 3' end /clone_end=3'	-1	AACTGGATAGAGCACGACCTTCTAA GCTTGGAGTTGCAAGTTTCAATCC
5646	db mining	Hs.279824	AW064185	8888122	SP0630 cDNA, 3' end /clone_end=3'	-1	GAAGATCGGCGCAACGAAGACCGCT TCCAATTGATCACTGGACCAAGAA
5647	Table 3A	NA	AW064187	8888124	(One single EST, artifact ?) SP0632 KRIBB Human CD4 Intrathymic T-cell cDNA library cDNA 3', mRNA sequence	-1	TGCTTCTGTGACAGATTAGCTTACAT CTTACCACCTCACCGAGAAGAGCT
5648	db mining	Hs.279146	AW064189	8888126	SP0634 cDNA, 3' end /clone_end=3'	-1	AGCTCAAGAGCTTCCGCGACGTACC CAGCAAAGTAACGCTCGACGAATGC
5649	db mining	Hs.279145	AW064194	8888131	SP0633 cDNA, 3' end /clone_end=3'	-1	ATCGAAGACGTGATGCTGAACCTTTG GGCGAAGGCCGAGAAGGAAGGCAA

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5650	db mining	Hs.279147	AW064201	8888138	SP0650 cDNA, 3' end /clone_end=3'	-1	CGATACCCCTCACTAGACCTCGGATCG AAATAAATCAGAGCGATACATCG
5651	db mining	Hs.279132	AW064208	8888145	SP0658 cDNA, 3' end /clone_end=3'	-1	GGGGATACACACCCCAAGCCTTC CTGCCGGCTTCATCAGGTTACCAACC
5652	db mining	Hs.279148	AW064218	8888155	SP0732 cDNA, 3' end /clone_end=3'	-1	GATCTTGGTGAGAGCTCGGTTCATGT AGAAGACCTCGCCCTGGGACACTA
5653	db mining	Hs.279826	AW064223	8888160	SP0676 cDNA, 3' end /clone_end=3'	-1	ATTTTATCGCCAGCTACGTCGGCATT GGTCAGGACGACCTGAAGGGGAAT
5654	db mining	Hs.279149	AW064250	8888187	SP1013 cDNA, 3' end /clone_end=3'	-1	TGATGCGGAGAGCGAGGTAGATCCC GGCGGAGTTTTCTCGATGGGAAAG
5655	db mining	Hs.279150	AW064255	8888192	SP0105 cDNA, 3' end /clone_end=3'	-1	GTACACTTCCTGGATCTGATCCACGA GGTAACGAGCGAGAGTGGTGATAC
5656	db mining	Hs.279134	AW064258	8888195	SP0717 cDNA, 3' end /clone_end=3'	-1	GTGACTTCATGCTCGGGGTTGAGCTT GGCGTCCACCACCTTTTCCCACTC
5657	db mining	Hs.279151	AW064272	8888209	SP0130 cDNA, 3' end /clone_end=3'	-1	CCGGTGTCTTGTATCAGCTTCAGCAG TGGCTTGACGTAGATCGGGTCCGG
5658	db mining	Hs.302427	AW064275	8888212	SP1065 cDNA, 3' end /clone_end=3'	-1	CATCAGTGTCTCTCTGCTGGGACTG TTGCATGTGGTGATCAGCTGGTTTG
5659	db mining	Hs.279153	AW064284	8888221	SP0755 cDNA, 3' end /clone_end=3'	-1	GCGAGGCGAAACATAGCTTCCATTGT GTCTTTTCTCCTTATGCGTCTTG
5660	db mining	Hs.279156	AW064319	8888256	SP1055 cDNA, 3' end /clone_end=3'	-1	AATGAGACCCGCGCTCCCTGGAGAT GAAGATGTCGTCGACCTCCGTCAC
5661	db mining	Hs.279157	AW064320	8888257	SP1045 cDNA, 3' end /clone_end=3'	-1	CGGATGTTGTCTTCCAGAACGAAG GATCGGCCTCTTGGCCCTGGATTTC
5662	db mining	Hs.279164	AW064343	8888260	SP0916 cDNA, 3' end /clone_end=3'	-1	GGCACCGACTTGGGCCTGAGAGAGG CGCAGGTCATCAATATAGAATCGGG
5663	db mining	Hs.279159	AW064348	8888285	SP1044 cDNA, 3' end /clone_end=3'	-1	CCATGCTGAACCTGGCCAGGTCTTG ACGGCGGTGTTTTCCGACAGCACC
5664	db mining	Hs.279161	AW064375	8888312	SP0115 cDNA, 3' end /clone_end=3'	-1	CGCGATGATCTCGCTTCGCGCATG GCGATGCGCTATTCTTCGACATGG
5665	db mining	Hs.279162	AW064377	8888314	SP1066 cDNA, 3' end /clone_end=3'	-1	GCCCATTGACCGTATCCGCTCATCTT GCTGGCATTTCTAAGAAAAATACCG
5666	db mining	Hs.279163	AW064378	8888315	SP0966 cDNA, 3' end /clone_end=3'	-1	TGAAACAGGGAAGGCGAGGAAGAT CTCCGGTTCCACGTCCAATTTGTAC
5667	db mining	Hs.279168	AW064424	8888361	SP1056 cDNA, 3' end /clone_end=3'	-1	CAAGAATGACGGAAGAAATCCGTGAGC ACAAGGCAAAGGCTTGCGGTGTGG
5668	db mining	Hs.279165	AW064433	8888370	SP1030 cDNA, 3' end /clone_end=3'	-1	GACTTGATCACAACCCGATCCGTAAC GACGTATTGGAGCCACTCGAACAA
5669	db mining	Hs.279166	AW064445	8888382	SP1042 cDNA, 3' end /clone_end=3'	-1	CTTCTCGCGTAACCTTTCCGCCGAG CAGCTACGACGCTAGGTGTTGTG
5670	db mining	Hs.279823	AW064450	8888387	SP1048 cDNA, 3' end /clone_end=3'	-1	TCGACTACGACTTCAACTTCCCAAAA CGGTGGGAGAAGCGAGCTTGAGGC
5671	db mining	Hs.279167	AW064452	8888389	SP1069 cDNA, 3' end /clone_end=3'	-1	AAGTTGATCAGATCAGGGGCCACGC CTGCAACAGAGGCTTGTCATCTGC
5672	db mining	Hs.279169	AW064468	8888405	SP1087 cDNA, 3' end /clone_end=3'	-1	TGATCTGATTGTGAGGAGAGTGGAGA AGGTGGTATAGAAGCTGAAAGGCT
5673	db mining	Hs.279155	AW064473	8888410	SP1072 cDNA, 3' end /clone_end=3'	-1	CTTCATGCTCGAGAAGAAATGCTCC GTGCCCTCCGACGACGCCACCATCG
5674	db mining	Hs.279170	AW064478	8888415	SP1080 cDNA, 3' end /clone_end=3'	-1	CAGATGGTACGAGACGCTTGTCGG TGATGTCTTCCGTCAGCGTGAGAG
5675	db mining	Hs.279171	AW064479	8888416	SP0147 cDNA, 3' end /clone_end=3'	-1	TGATGGATTGGAAAGTGTTATTCTG TTGACTTCTCCCTGCTCTGCTCA
5676	db mining	Hs.279158	AW064487	8888424	SP1087 cDNA, 3' end /clone_end=3'	-1	TTGAACGGGTATAGCCACCAAGGCAT TGGCTGCAAAGTCGGGCAAAACTT
5677	db mining	Hs.330544	AW064490	8888427	SP1090 cDNA, 3' end /clone_end=3'	-1	ACTGTGATTGATGAGTATCTGATGC CTATAACATCTGTAGGAGGCTACA
5678	db mining	Hs.279160	AW067725	8888472	SP0110 cDNA, 3' end /clone_end=3'	-1	GTACGAAGGTGGCGATGATGCGTTT GTACACCTCGGGGATTTCCTCGGCG
5679	db mining	Hs.279129	AW067742	8888489	SP0150 cDNA, 3' end /clone_end=3'	-1	CGACCTTCGGCGTTTCCGCTTCGGAA CCCGTGAAGGCGTTCTTCACTTTG
5680	db mining	Hs.279133	AW067752	8888499	SP0141 cDNA, 3' end /clone_end=3'	-1	ATTCGCTGGCAACATAATTACGAGAC TCACATCGAACGAAGCTCGGTTCC
5681	db mining	Hs.279154	AW067760	8888507	SP0122 cDNA, 3' end /clone_end=3'	-1	TGTTCTGTTGCCATCTTGTGAGGAA CATCTCGCTTTCAGTTCCGCTG
5682	Table 3A	Hs.89433	AW071894	6026892	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791)	-1	TTTGGGGGATCCTTTTGTATGACTT ACACTGGAATGCGAACATTGCA
5683	Table 3A	Hs.299581	AW073707	6028705	xb01h03.x1 cDNA, 3' end /clone=IMAGE:2575061 /clone_end=3'	-1	GGACAAGGGGACCCGGATTATATT CCCACCAATCTAATCTAAACCC
5684	db mining	Hs.243286	AW075809	6030807	xa85g05.x1 cDNA, 3' end /clone=IMAGE:2573624 /clone_end=3'	-1	TGGAGCTTATTTTGGAGAACTGTAC CATTTTATCCAGTTGGCAATTTT
5685	db mining	Hs.277714	AW075814	6030812	xa85h03.x1 cDNA, 3' end /clone=IMAGE:2573621 /clone_end=3'	-1	ATTATGGGTAAGGCTTGGGCTTGTTC CCACATGTTAACCAAATGGCCTCA
5686	db mining	Hs.244048	AW075894	6030892	xa81c04.x1 cDNA, 3' end /clone=IMAGE:2573190 /clone_end=3'	-1	GGGAGGGGCCAAAGAAATCTTTTCCC GTTTCAAATTATGTTCCCAAAAA

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5687	db mining	Hs.329433	AW075905	6030903	xa81d05.x1 cDNA, 3' end /clone=IMAGE:2573193 /clone_end=3'	-1	TTACCCCAATGCTTTTGCCCCGGTGG CCCAGTTTGTAATTTGGTTTGATT
5688	db mining	Hs.329434	AW075921	6030919	xa81f04.x1 cDNA, 3' end /clone=IMAGE:2573215 /clone_end=3'	-1	CCCCCCTTGGCAGGTAAATTTGGTGT TAAGGAACCCCTCCAGGGTGGGGGG
5689	db mining	NA	AW075929	6030927	xa81g05.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2573240 3', mRNA sequence	-1	CCCCCAGTTTAAATGTTAGGGGGAA GGGATTTAACCCTTATTTAAAAAA
5690	db mining	Hs.265634	AW075948	6030946	xa82b03.x1 cDNA, 3' end /clone=IMAGE:2573261 /clone_end=3'	-1	CTATCACCCCTTGATATGAAATTCAG AATTTCTGTGATACCACATGGCC
5691	db mining	Hs.277716	AW075986	6030984	xa82f05.x1 cDNA, 3' end /clone=IMAGE:2573313 /clone_end=3'	-1	ACTCCGGGCCTTAATGGATTGCGCT GTCCTCAAGAATGGTAATTATGAA
5692	db mining	Hs.241982	AW076004	6031002	xa82h04.x1 cDNA, 3' end /clone=IMAGE:2573335 /clone_end=3'	-1	ACGTGGTTTCAGTCCTTAGCACCGTG GTATTGACATGACATCAGTTGCAA
5693	db mining	Hs.257711	AW076027	6031025	he31c12.x1 cDNA, 3' end /clone=IMAGE:2920630 /clone_end=3'	-1	CACAACCTTGCTGTTTACGCTTTTGGG GTGTTTCCATTCTTAATAGATGG
5694	db mining	Hs.277717	AW076038	6031036	xa83d08.x1 cDNA, 3' end /clone=IMAGE:2573391 /clone_end=3'	-1	AAACCCGCTCCTCATTATAATTACCTT TCAAAGGGCAAGTCAAAGTTGT
5695	db mining	Hs.241983	AW076068	6031066	xa84a02.x1 cDNA, 3' end /clone=IMAGE:2573450 /clone_end=3'	-1	AAACAGCACACATGAGTGTTCCTA CCACATCAATTTAATGAAGACAC
5696	db mining	Hs.277718	AW076075	6031073	xa84a10.x1 cDNA, 3' end /clone=IMAGE:2573466 /clone_end=3'	-1	CGGAATCGGGTTTCCATTGAGCCCA AAAATTTCCCTTTGGGCTTCATGA
5697	db mining	Hs.242605	AW076083	6031081	xa84b10.x1 cDNA, 3' end /clone=IMAGE:2573467 /clone_end=3'	-1	TGAGGATAGAAGCAGCCTTTTATATT TTTGTGTGGTAAAGCAAATGGCA
5698	db mining	Hs.329436	AW076127	6031125	xa84g01.x1 cDNA, 3' end /clone=IMAGE:2573520 /clone_end=3'	-1	GGGGCAAATTTCAAGGACCTCCCC AAAGGGGGTGTTCCTGGATGGG
5699	Table 3A	Hs.244816	AW078847	6033999	xb18g07.x1 cDNA, 3' end /clone=IMAGE:2578700 /clone_end=3'	-1	AAACAGGAAGGGGGTTTGGGCCCTT TGATCAACTGGAACCTTTGGATCAAG
5700	Table 3A	Hs.245616	AW080951	6036103	xc28c10.x1 cDNA, 3' end /clone=IMAGE:2585586 /clone_end=3'	-1	ACTCTTTGCTTTTTAAGACCCCTAAT AGCCCTTTGTAACCTGATGGCTT
5701	Table 3A	Hs.176488	AW081098	6036250	xc29a12.x1 cDNA, 3' end /clone=IMAGE:2585682 /clone_end=3'	-1	CCGGTGCGCTCCATCCAGAAAGAGT GCGCAGAGAATTAATCTAGATATT
5702	Table 3A	NA	AW081232	6036384	xc22e08.x1 NCI_CGAP_Co19 cDNA clone IMAGE:2585030 3' similar to SW:RS1A_HUMAN P39027 40S RIBOSOMAL	-1	GGGATGTAATACATATTTTCCAAATA AAATGCCTCATGGGCTTTGGGGC
5703	Table 3A	Hs.295945	AW081320	6036472	xc30f12.x1 cDNA, 3' end /clone=IMAGE:2585807 /clone_end=3'	-1	AGAACCCGTATTCAAAAAATTTAGAC CAAAAAGGAAGGAATCGAACCCCC
5704	Table 3A	Hs.120219	AW081455	6036607	xc31c07.x1 cDNA, 3' end /clone=IMAGE:2585868 /clone_end=3'	-1	AGTTAGTATACAGCCAGAACGCCAA GCCTCAATTCCTGTACCTGTGTC
5705	Table 3A	Hs.277738	AW082714	6037866	xb81f07.x1 cDNA, 3' end /clone=IMAGE:2580805 /clone_end=3'	-1	CCCTGATCCTCTGTAGGGAATTCCT TTTCTCTAATCCTAGATCTTTTCA
5706	db mining	NA	AW088500	6044305	xd10a04.x1 NCI_CGAP_Ov23 cDNA clone IMAGE:2593326 3' similar to SW:BAT3_HUMAN P46379 LARGE PROLINE	-1	GAGGCATCAGAGGTTACAGAGAGTT ACAGGCAGCAGGTGCGGTATAATAT
5707	Table 3A	Hs.243457	AW102836	6073449	xd38h12.x1 cDNA, 3' end /clone=IMAGE:2596103 /clone_end=3'	-1	TTTGTTCCTTTGGGCTGATTTGTATC TCTGGAAGGCATTAATCTTGAA
5708	Table 3A	Hs.341908	AW117189	6085773	xd83f08.x1 cDNA, 3' end /clone=IMAGE:2604231 /clone_end=3'	-1	GCTTTCCTCTCGGAGGAGTCAAAG GGGCAGTAACCTGTATGGGGTGAGAG
5709	Table 3A	Hs.3642	AW130007	6131612	RAB1, member RAS oncogene family (RAB1), mRNA /cds=(50,667)	-1	GCTCCCAATATTGTAATTTGTTGCC CCCTATGTACCAACCCCTGAAA
5710	Table 3A	Hs.248367	AW131768	6133375	MEGF11 protein (MEGF11), mRNA /cds=(159,3068)	-1	AGGAAGTATGAGAGTTCTGAAACCTT TGATAGAACTGGAAGCCTGCCAT
5711	Table 3A	Hs.203608	AW131782	6133389	PMO-UT0103-300101-002-f12 cDNA	-1	GACATAGGGTTGCAGTAGTGAGTGG GCATCTGTTCTCAGAAGGCAGTGCC
5712	Table 3A	Hs.335449	AW136717	6140850	UI-H-BI1-adm-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2717092 /clone_end=3'	-1	TTCTGGCCTTGTTCACCTAGAAACGC TATTCCTGTGTATGTGTTCTGGC
5713	Table 3A	Hs.8121	AW137104	6141237	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	-1	GCTCTGGGAAAGAGACAGGGAAGTC TGGAATGGAAAAGAACACGATGAGA

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5714	Table 3A	Hs.12035	AW137149	6141282	602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5'	-1	GGGTACATTGAGTCTCTGTACCTG CTTGGAGAAATAAAAAACGCTGT
5715	Table 3A	Hs.342003	AW138461	6142779	UI-H-BI1-adg-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2716882 /clone_end=3'	-1	CTGGGAATATGAAGCGAACGCCACA CACTAGAACGCGCCCTGGGAGCTGG
5716	Table 3A	Hs.245138	AW139918	6144636	UI-H-BI1-aee-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719136 /clone_end=3'	-1	GCTGCTTTTGGCCCATCCAGGTTTCCA CATCCTAATCTTTGCTTTTCTTGT
5717	Table 3A	Hs.276718	AW148618	6196514	601473284T1 cDNA, 3' end /clone=IMAGE:3876165 /clone_end=3'	-1	TGTAAATGTGGTTTGACTATTTCTGTA TGTCCCCATCTATTGATGAGGGT
5718	Table 3A	Hs.89104	AW148765	6196661	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TTGTTTTAAACACTCTTCTCAACATT TGTCCAGGTATTCTACTGTAAACCA
5719	Table 3A	Hs.248657	AW150084	6198076	xg36f03.x1 cDNA, 3' end /clone=IMAGE:2629661 /clone_end=3'	-1	ACATAAACTGTCCTTTAGGAAGAAG CCCAATGCCCGATTTTGCCCTTTA
5720	Table 3A	NA	AW150085	6198077	xg36f04.x1 NCI_CGAP_UH1 cDNA clone IMAGE:2629663 3' similar to gb:X65018 PULMONARY SURFACTANT-ASSOC	-1	GGACAAGTGGCATCGGTACTATATTT CCCACCAATCCTAATCCTAATCCC
5721	Table 3A	Hs.265838	AW150944	6198842	xg42e09.x1 cDNA, 3' end /clone=IMAGE:2630248 /clone_end=3'	-1	TATGTCCCTTTTCTCCTCCCTCCCC ATTCCCTGGCATCATATTGGGAC
5722	Table 3A	Hs.301104	AW151854	6199839	602313002F1 cDNA, 5' end /clone=IMAGE:4422480 /clone_end=5'	-1	CGCTGTGCGCTTAATCCAAGCCTACG TTTTCACACTTCAGTAAGCCTCT
5723	Table 3A	Hs.337727	AW161820	6300853	au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3'	-1	TGTGGGCTTGGTATAAACCTACTTT GTGATTGCTAAAGCACAGGATGT
5724	Table 3A	Hs.299967	AW166001	6397528	x43e11.x1 cDNA, 3' end /clone=IMAGE:2620844 /clone_end=3'	-1	CCGCCTGAAACGGGCATTTTGTAAAT GGGGTTTGACTATTTTGTATGTC
5725	Table 3A	Hs.81248	AW166442	6397967	CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585)	-1	ACTGGCAAATGAAGCATACTGGCTTG CAGGGACCTCTGATTCAAGTACA
5726	Table 3A	Hs.169738	AW172306	6438254	xj37a08.x1 cDNA, 3' end /clone=IMAGE:2659382 /clone_end=3'	-1	GAATTCGATTTGAGATCTGAGGGCAG ACCCGAACCAGGAAAGCAACTCAG
5727	Table 3A	Hs.8991	AW172850	6438798	adaptor-related protein complex 1, gamma 2 subunit (AP1G2), mRNA /cds=(45,2402)	-1	AATGCACCAGGCTGCCACCTGCACC AGTGGTGTCTACATGGGATAAGAAA
5728	Table 3A	Hs.143525	AW173183	6439111	xj84b08.x1 cDNA, 3' end /clone=IMAGE:2663895 /clone_end=3'	-1	TATGATAGGATTCTCCACAGTGGCTT CCGACTCAGGCTCCAATGGACCAA
5729	Table 3A	Hs.38664	AW188135	6462571	IL0-MT0152-061100-501-e04 cDNA	-1	TGCTGTATGGGCAGGTTGTCTTATTA TGTGATCAACAGATGTCCAGGAAC
5730	Table 3A	NA	AW188398	6462834	xj98c03.x1 NCI_CGAP_Co18 cDNA clone IMAGE:2665252 3', mRNA sequence	-1	ACCTCCAAGAATCTGCCTTTGTTG AACGTGTTTATTACCTGTCCACTC
5731	Table 3A	Hs.252989	AW191929	6470628	x77c10.x1 cDNA, 3' end /clone=IMAGE:2680722 /clone_end=3'	-1	CCTTTTGGCCCTTAGCCCTTGGATAA TCCGGCTGGGAATGGGGTGAGGG
5732	Table 3A	Hs.203755	AW194379	6473179	xm08h07.x1 cDNA, 3' end /clone=IMAGE:2683845 /clone_end=3'	-1	CCCAAATAAGCTCTGTACTTCGGTTA CCTATGTACTGTATACCACTTCA
5733	Table 3A	Hs.253151	AW195119	6474139	xn66b07.x1 cDNA, 3' end /clone=IMAGE:2699413 /clone_end=3'	-1	GCCACATGTCCTATTCTCACACAGGT GCTTTAATTTACGCCAGTCTCTA
5734	db mining	Hs.253154	AW195169	6474211	xn66h03.x1 cDNA, 3' end /clone=IMAGE:2699477 /clone_end=3'	-1	CTTGAAGGGGCTTTGTTGGGTTTTTG GGTTTTTGGGTGGGACTCCCAAAG
5735	db mining	Hs.330019	AW195270	6474330	xn67c04.x1 cDNA, 3' end /clone=IMAGE:2699526 /clone_end=3'	-1	GGGGTTTTAAAAATTTCCCGATTCA AAATTAATTTTCCGTTGCCCCCGG
5736	db mining	Hs.253167	AW195284	6474352	xn67d09.x1 cDNA, 3' end /clone=IMAGE:2699537 /clone_end=3'	-1	CCCCCTGGGGTTTTTGGGAATGAGG TAAGGCTTTGAATTTGGTTTGATAT
5737	db mining	Hs.253188	AW195300	6474368	xn67f12.x1 cDNA, 3' end /clone=IMAGE:2699567 /clone_end=3'	-1	ACATGCTTAGAGCTGGAGGCTTGAAA CCATAATCCCAATTAAGTGCTGTC
5738	db mining	Hs.253169	AW195313	6474381	xn67h05.x1 cDNA, 3' end /clone=IMAGE:2699577 /clone_end=3'	-1	TGTTTGTCCAGGAAAAGGAAGAGGG GGAAATTAAACCTTTCCGGTTAGT
5739	Table 3A	Hs.253384	AW204029	6503501	UI-H-BI1-aen-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2719899 /clone_end=3'	-1	GCACTGCTCCGCTAGCTGTATGACC TTTGTATGTTTCTTTCTTCCGT
5740	Table 3A	Hs.253502	AW205624	6505098	UI-H-BI1-af-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2722657 /clone_end=3'	-1	CTTCAATCTGGGCTGGGCACTCCAC GCACATAATCGTCACTCTCGGAGGA

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5741	Table 3A	Hs.330058	AW206977	6506473	UI-H-B11-afs-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2723180 /clone_end=3'	-1	GCGGGGAAGTGAAGCGGAGGCTGGG ACAAGGGGAACCTTACTGCTCAAAAA
5742	Table 3A	Hs.157315	AW207701	6507197	UI-H-B12-age-e-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724172 /clone_end=3'	-1	AGTGGTGTGGTGGCAATAGGAAAAG AAAAGATCAGGATGAGAAATTGCTT
5743	db mining	NA	AW236186	6568575	xn70e07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699844 3', mRNA sequence	-1	CCAAGGGCCCTTTTGGGGTGTTCCT ATAACTTCAGTATTGTAAATTAGT
5744	db mining	NA	AW236203	6568592	xn70h07.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2699869 3', mRNA sequence	-1	CATAAAGGGGCATTGCCCTAGCCGG TCCGGCCTTTTCCAGTCCATCCTG
5745	db mining	Hs.330063	AW236208	6568597	xn71a06.x1 cDNA, 3' end /clone=IMAGE:2699890 /clone_end=3'	-1	AGGTTTAAGAAATTTCCCTAAATCTT GTTTGGTTGGTTGGGATGAAAGT
5746	db mining	Hs.253747	AW236252	6568841	xn71g08.x1 cDNA, 3' end /clone=IMAGE:2699966 /clone_end=3'	-1	AATTGATCCCATTCTTGCTGAAGTAG ACAGTCCCTCAAGTGAATTAATA
5747	db mining	Hs.253748	AW236271	6568660	xn72b03.x1 cDNA, 3' end /clone=IMAGE:2699981 /clone_end=3'	-1	CTCCAATGCTGTTATCCCGCTGGGT CCTCACTCCCCCAACATCCCA
5748	db mining	NA	AW236345	6568734	xn73c12.x1 NCI_CGAP_CML1 cDNA clone IMAGE:2700118 3' similar to contains element MER21 repetitive e	-1	AGAATGCGCTATTTCCCTCAAAGCCC TGGCTGTAATAAGAACGCCGATT
5749	Table 3A	Hs.253820	AW237483	6569872	xm72e01.x1 cDNA, 3' end /clone=IMAGE:2689752 /clone_end=3'	-1	CTGAGGTCAGTGTGGTTTGGTGGA GGATTATGATATTTACAAGCTGAGT
5750	Table 3A	Hs.342342	AW243795	6577635	xo56f02.x1 cDNA, 3' end /clone=IMAGE:2707995 /clone_end=3'	-1	GGTCAATGTTTTGAAATTTGTGGAGC AAACCCAGTTTTATGCCCTTGGT
5751	Table 3A	Hs.250591	AW262077	6638893	xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3'	-1	AGTTGGAAATTTAGAAATGTCCACT GTAGGACGTGGAATATGGCGTCGA
5752	db mining	Hs.250591	AW262272	6639088	xp19e09.x1 cDNA, 3' end /clone=IMAGE:2740840 /clone_end=3'	-1	TTCACGTCCTAAAGTGTGGTAGACGC GCCCGCGAATTTAGTAGTAGTAGG
5753	Table 3A	Hs.277994	AW262728	6639544	xq94a12.x1 cDNA, 3' end /clone=IMAGE:2758270 /clone_end=3'	-1	GGACAAGTGGCATCCGTATTATATTT CCCACATTCTCTATTCTTAATCCC
5754	db mining	Hs.61345	AW262891	6639707	mRNA for KIAA1154 protein, partial cds /cds=(0,676)	-1	GGTCTGCCTCAGTCTTCTACTCATCA GCACCCACTGTCAAAATGTTGGA
5755	Table 3A	Hs.5662	AW264291	6641033	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(95,1048)	-1	AGATGAATTGAAGCAAAAGTTTCA GTACCAGCAGCAAGGCAGACCCCC
5756	Table 3A	Hs.122655	AW274156	6661186	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686)	-1	TCACCTCCACCTCTGAGGGAGCAAC GAATACAAAGGTAGACCCCCAAAAG
5757	Table 3A	Hs.250600	AW291304	6697940	UI-H-B12-agk-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724386 /clone_end=3'	-1	CCCCAGCCAGCACTTCCCTTTTCTGC GAGGGTTTCTGTTCTTTGATTA
5758	Table 3A	Hs.47325	AW291458	6698021	UI-H-B12-agh-c-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2724099 /clone_end=3'	-1	AGAAAAATTTGAACCCACGCTTCTCC CATCCCACTTCTTACTCCATCCCG
5759	Table 3A	Hs.170381	AW291507	6698143	UI-H-B12-aga-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2723900 /clone_end=3'	-1	CTGTGGCATCATTACACCACAGCA GAGTCCCTTCCAAGAGGGGTCTGG
5760	db mining	Hs.255118	AW292757	6699393	UI-H-BW0-aij-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729423 /clone_end=3'	-1	CCGTGTTAAAAACCAAGTTTGGGATT TTTCGGGTATTCATTGGAAGTCAC
5761	Table 3A	Hs.255119	AW292772	6699408	UI-H-BW0-aij-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729501 /clone_end=3'	-1	CGAGAGCCTGGAAGCTTTGCACACTA CTGCCTGGAAGATCTGATTCTTTG
5762	db mining	Hs.255123	AW292814	6699450	UI-H-BW0-aij-h-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729691 /clone_end=3'	-1	TGTTTTAAAGTGGGTTTATTTCAACC CCTTCACTCCCGGTTGGTGACCG
5763	db mining	Hs.255129	AW292855	6699491	UI-H-BW0-aij-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729117 /clone_end=3'	-1	TCTTCTCTCAGTCTTCAGCAAGTAGC TTCTTTCAGAACTGCCTCCTCCCG
5764	db mining	Hs.255544	AW292873	6699509	UI-H-BW1-ame-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069784 /clone_end=3'	-1	GTTTTCTGCATCCCAATGTCCTGGG GCATGTGCTCCCTTCTTGCTGACC
5765	db mining	Hs.255134	AW292900	6699536	UI-H-BW0-aig-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729000 /clone_end=3'	-1	TGTTATGATTCTCTCAATTTATAAAG CTCTTCTGGCAGAGGAGACAGAT
5766	db mining	Hs.255135	AW292902	6699538	UI-H-BW0-aig-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729004 /clone_end=3'	-1	AAATGGATTACAAATTTCCCTGACATT GGGCATAAACATCTGCCATCCT
5767	db mining	Hs.255139	AW292928	6699564	UI-H-BW0-aig-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729156 /clone_end=3'	-1	TCCTCCTTCCAGAGACCTTTGCTTTA CTGCCATTTTTCTGTGGGCTTTT
5768	db mining	Hs.255140	AW292941	6699577	UI-H-BW0-aig-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729250 /clone_end=3'	-1	AGGCATAGCAGTAGAATCTGTCAAAA AGGAGGCATGGAATGAAATGAACC

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5769	db mining	Hs.255142	AW292980	6699596	UI-H-BW0-aih-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728995 /clone_end=3'	-1	CTGACCCCTCTCGCCCTCCACCTGTG CTTCTGCCCTAGGATAACGCTGGG
5770	db mining	Hs.147728	AW292989	6699625	RST12623 cDNA	-1	GACCCAAAGAAAGATCAAGACCGCA TGTAGCAAATGTAGCAAGGAGGCA
5771	db mining	Hs.255152	AW293001	6699637	UI-H-BW0-aih-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729159 /clone_end=3'	-1	CTAATTTCCCACTAAAAGGTCCAGAA AAATTGATGCCACCTGTAGTTTGG
5772	db mining	NA	AW293017	6699653	UI-H-BW0-aih-f-06-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729243 3', mRNA sequence	-1	GTAAGTTCCAAGCGAGTGGAAGGTA AATCAGCACTGTGGCACC GGAGGCC
5773	db mining	NA	AW293143	6699779	UI-H-BW0-aih-a-03-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2729356 3', mRNA sequence	-1	GAAACTGAATGACCATGGAATGCTGA AATTCCAAAAGAAAACGTCGCCGC
5774	db mining	Hs.255172	AW293158	6699794	UI-H-BW0-aih-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729412 /clone_end=3'	-1	TCTCTCAGGTCGTCTTCAGAGTCCAT TCCCTTTGTCTTATCTTTTCTCT
5775	Table 3A	Hs.166975	AW293159	6699795	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541)	-1	CTCCCATCATTCCCTCCCGAAAGCCA TTTTGTTCAAGTTGCTCATCCACGC
5776	db mining	Hs.255174	AW293172	6699808	UI-H-BW0-aih-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729466 /clone_end=3'	-1	GCCCTGCCCCCTACCCTTGCCCTTTA AATTTTTGGGACTGAATAAAGAAT
5777	Table 3A	Hs.255178	AW293267	6699829	UI-H-BW0-aih-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729562 /clone_end=3'	-1	TGCAGGATAACTTGCTCATGAAGGA AATGCCAGATTAAACCCCTTGCCA
5778	Table 3A	Hs.75354	AW293424	6700060	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	-1	GCCTTCCCTTCGTTCTTCCAGGCA ATAATGACATCATTAGTGATGCAA
5779	Table 3A	Hs.255200	AW293426	6700062	UI-H-B12-ahm-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2727122 /clone_end=3'	-1	CGCCACGGCTCCAATCCCTATATGAG TGAGCAGTAGAATCACATAGGAAT
5780	Table 3A	Hs.10041	AW293461	6700097	602713308F1 cDNA, 5' end /clone=IMAGE:4853616 /clone_end=5'	-1	CCTAGAATCAGACTTTAAGCACAAGC AGGGAGGGAAAGCACTTGAGCAGT
5781	db mining	Hs.291317	AW293859	6700495	nx40e10.s1 cDNA, 3' end /clone=IMAGE:1258602 /clone_end=3'	-1	GCACATGCAAAAACCTCAGATGTGCAA ATAACTGTTCCCTATTAACTACAA
5782	Table 3A	Hs.255249	AW293895	6700531	UI-H-BW0-aih-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729995 /clone_end=3'	-1	GGTGCTCAAACGTGATTTTCTCCCTC CCTCCCTCCTCTTTCTTTCCAGA
5783	db mining	Hs.255251	AW293922	6700558	UI-H-BW0-alk-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729382 /clone_end=3'	-1	TTCTTCCACGGGATTTCTAATTCATTA AATAGGACCTCCACACCAGACCT
5784	db mining	Hs.255253	AW293949	6700585	UI-H-BW0-alk-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729490 /clone_end=3'	-1	TATCCAGCCTGACTTCTTCATGCTGT ACTAGCCTTCCAATCCCTAACTAA
5785	db mining	Hs.255254	AW293950	6700586	UI-H-BW0-alk-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729492 /clone_end=3'	-1	TGGACATTGGGGGTCAAACCCCTTTTG TTTAAATTTTCCCTTCCAGGGC
5786	Table 3A	Hs.255255	AW293955	6700591	UI-H-BW0-alk-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729528 /clone_end=3'	-1	GCTGTGCCACGGTCAGGTGGCTTCC AATCTGTACTCAATTGTTACTGTAC
5787	Table 3A	Hs.190904	AW294083	6700729	UI-H-B12-ahg-b-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726720 /clone_end=3'	-1	TCAGAGATGCTGATGTCATATAAGTA GTTTCCCTGTCTGGCCTTGGATGT
5788	db mining	Hs.255330	AW294618	6701254	UI-H-BW0-aih-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729385 /clone_end=3'	-1	GTATGACTGATGATAGCTGCGAATGA GGAGGAGGGAAGGGAAGGCTGGAG
5789	db mining	Hs.255333	AW294644	6701280	UI-H-BW0-aih-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729493 /clone_end=3'	-1	CCATTGCCCGGTGTTTGTGTTTAAT TTTCCAGGCTTATTTTAAAGGCC
5790	Table 3A	Hs.255687	AW294654	6701290	UI-H-BW0-aih-d-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729539 /clone_end=3'	-1	AGGAAATTAACATGAGCATGACATG ACCCCAACTCTCAAGAAATCCCCA
5791	Table 3A	Hs.255336	AW294681	6701317	UI-H-BW0-aih-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729683 /clone_end=3'	-1	ATCAGGTCCCCTACAAAATTAGCTAC TTTGCCCTTCTCTACAAAATTAGC
5792	db mining	Hs.255337	AW294692	6701328	UI-H-BW0-aih-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729733 /clone_end=3'	-1	TCATTCTGTTTCTTCTCTGACTGACA GGCAGTAATGACTTCAATAAGCT
5793	Table 3A	Hs.255339	AW294695	6701331	UI-H-BW0-aih-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729738 /clone_end=3'	-1	AGGGCCTGCTTCAGAGTTTGTTCCT AAATAAACAAATGGCTCTCCCCGT
5794	db mining	Hs.255341	AW294697	6701333	UI-H-BW0-aih-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729742 /clone_end=3'	-1	CCCCCAACTTACATGGAAAAGGGATG GTTGCATTTCTGTGCATATGCAT
5795	db mining	Hs.342539	AW294717	6701353	UI-H-BW0-aih-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732333 /clone_end=3'	-1	GCAGAGGGAAGAGGAAATGCTTTGA AGCCTTGCTAGTTATTTAATTAGTT
5796	db mining	Hs.255347	AW294739	6701375	UI-H-BW0-aih-f-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729988 /clone_end=3'	-1	GACATAGTTGCAAAACACAATACTTA ATACTTTTTCTGGAGGAGGGGGCC

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5797	db mining	Hs.255354	AW294769	6701405	UIH-BW0-aii-g-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:2729667 /clone_end=3'	-1	ACCCCTTTTCTTAATTTCTCAGGAAAA TGGCAGCTCCTTCTTTTGTCTGTC
5798	db mining	NA	AW294812	6701448	UIH-BI2-ahi-d-06-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2726842 3', mRNA sequence	-1	CCTCCGGTGTCTTCGGAAGCACTGAA GGGACATCTGGGGACCCCTCACCTG
5799	db mining	Hs.255388	AW295071	6701707	UIH-BW0-ait-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730245 /clone_end=3'	-1	ACTCTTTGACCAATAAATCACTGGAA TAGAGGTTCCAGCATATTCTGAGA
5800	Table 3A	Hs.255389	AW295088	6701724	UIH-BW0-ait-d-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730305 /clone_end=3'	-1	ATGCTTACACCCTGGATGAATAAAGT CTTTATTTACACCTCCACCTCCCC
5801	db mining	Hs.255157	AW295376	6702012	UIH-BI2-ahv-f-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728085 /clone_end=3'	-1	CTCTTCACAGGTCATAAGCCCCTCTG AGCGGCGACAGTCTCCGATCCAG
5802	db mining	Hs.330175	AW295597	6702233	UIH-BW0-aip-a-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729779 /clone_end=3'	-1	CAGCTCGACCTCAGTCCCCTTCAGAA ATAAGATGGCGCTGCGCTGACAG
5803	Table 3A	Hs.255446	AW295610	6702248	UIH-BW0-aip-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729861 /clone_end=3'	-1	TTTCAACGTGTACCTTTCTGGGAAA CCATCTCAATAAAGACATTTTGGT
5804	db mining	Hs.255448	AW295616	6702252	UIH-BW0-aip-c-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729873 /clone_end=3'	-1	GCTGGACACATGGGTTAAGAGGAGG AAAAGTAGGAAAGGAGGAGGGGAAA
5805	db mining	Hs.255449	AW295629	6702265	UIH-BW1-amu-a-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071128 /clone_end=3'	-1	GGCTGGGACCAGGGTTTTTCAAGCC ACCTTTTCTGTCTCAGTTCAGAGA
5806	Table 3A	Hs.255454	AW295664	6702300	UIH-BW0-aip-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730071 /clone_end=3'	-1	CCCACCTTCACACATGACTCACACGA CTGAAGGAAAGAAAGGGCATCCTT
5807	db mining	Hs.255455	AW295669	6702305	UIH-BW0-aip-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730107 /clone_end=3'	-1	AAGAAATTAAGGAAGGCAAGAGGGTA GGTGTGGCCCATGGAAGTTTCCC
5808	db mining	Hs.255457	AW295688	6702324	UIH-BW0-aiw-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730578 /clone_end=3'	-1	CTGGCAAATATTGCGGAAGATGTACT GAAATGTAATTGAAATGTAGCTGC
5809	db mining	Hs.255459	AW295711	6702347	UIH-BW0-aiw-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730676 /clone_end=3'	-1	AGCATAAGAGATACGAAGCTGATGGT AATTAACCTGTACCCCTTGAAGTG
5810	db mining	Hs.255462	AW295724	6702360	UIH-BW0-aiw-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730734 /clone_end=3'	-1	AGTGTGACACAATTAGATACTCTTTC CTGTCTTCAGGAGCCCATCTGGAA
5811	db mining	Hs.255464	AW295731	6702367	UIH-BW0-aiw-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730776 /clone_end=3'	-1	GAAGTGTAACATGCCAACAGGGTTT ATATTTAGGTTCCAAGAGTTGCCA
5812	Table 3A	Hs.156814	AW295965	6702531	KIAA0377 gene product (KIAA0377), mRNA /cds=(126,4346)	-1	CTTCCCAAACCTCATTGTCTCATTCTC ACTGCTTATGTTATTGCTCTTAT
5813	Table 3A	Hs.255492	AW296005	6702641	UIH-BW0-aiw-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730552 /clone_end=3'	-1	CCCACACAGCAGAGAAGTATCAGAAA ACATAGAAACATGTGAAAATGCCG
5814	db mining	Hs.255495	AW296020	6702656	UIH-BW0-aiw-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730612 /clone_end=3'	-1	AGGTTCAATTCATTTCTGAGATGTT TGGTTTATAAGATTGAGGATGGT
5815	db mining	Hs.255497	AW296044	6702680	UIH-BW0-aiw-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730714 /clone_end=3'	-1	ATACTTAGATGTGCTTGGATCTGGG TGGGAGGCTTGGTTAGAAGTCACG
5816	db mining	Hs.255498	AW296054	6702690	UIH-BW0-aiw-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730762 /clone_end=3'	-1	TGGGTGAGCGTGTTCATTTTAAATA GGAATACACTAGCCCTTACAACGGA
5817	db mining	Hs.255499	AW296058	6702694	UIH-BW0-aiw-g-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730794 /clone_end=3'	-1	TGTTCACTTGATGTAATAGAGAAGG AAGAGAGAGCATCCCTTTTCAGT
5818	Table 3A	Hs.255501	AW296063	6702699	UIH-BW0-aiw-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730806 /clone_end=3'	-1	ACCAGTAACACAATGACGGCAAGCAC AGAGAAGGAAAAAGTCAGATCCCC
5819	db mining	Hs.255502	AW296066	6702702	UIH-BW0-aiw-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730812 /clone_end=3'	-1	ACTTGGAGCTAGAGGCCACCCATCA TATGGAGGAGAAGTGGTCACTCTA
5820	db mining	Hs.34871	AW296352	6702988	zinc finger homeobox 1B (ZFX1B), mRNA /cds=(444,4088)	-1	TGCATGTGTGTGTGTACTTGTCTGT TCTGTAAGATTGTCGGTGTACAC
5821	db mining	Hs.255543	AW296373	6703009	UIH-BW0-aio-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729874 /clone_end=3'	-1	TTCTGGCAGTAAAGAAAAGAAAGAA GATGTGAGTTATGAAGCATTGACT
5822	db mining	Hs.255546	AW296398	6703034	UIH-BW0-aio-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730000 /clone_end=3'	-1	AAATAGGAATATAATCTGTCCACATC AAAGAATGGGAAGTCGAAGTGTACA
5823	db mining	Hs.255549	AW296404	6703040	UIH-BW0-aio-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730014 /clone_end=3'	-1	GTTCCAAATGTTTTCCGCTAATAGTTT GTCCTAAAGCCTTTGCCATTCCT
5824	db mining	Hs.255552	AW296446	6703082	UIH-BW0-aio-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730180 /clone_end=3'	-1	ACAGAGAAGGCTTATTACGTTGGGA ATTACATTAAAGGAAAAGTGGTGAC

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5825	Table 3A	Hs.255554	AW298480	6703128	UI-H-BW0-aiq-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730374 /clone_end=3'	-1	CCTTCCTCCTATATCTGCCTTGAAT AGGGATGTGATACCTTGAGCCATG
5826	db mining	Hs.255556	AW298504	6703140	UI-H-BW0-aiq-g-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730430 /clone_end=3'	-1	ATATTTGGGTCTCTGTTTAAGATTTC TTGCCGTGGTAGGGAGAGTTCCA
5827	db mining	Hs.255558	AW296511	6703147	UI-H-BW0-aiq-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730470 /clone_end=3'	-1	TGGATGCCATGATGACACCAATAAGC AACCACAGATTAGGGGAAATACT
5828	Table 3A	Hs.255559	AW296532	6703168	UI-H-BW0-aiq-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730585 /clone_end=3'	-1	GGGGCTGGGAGCCACCAAAGGGCC TGCTCTTGGGAGAAATGCTGAATTC
5829	Table 3A	Hs.255560	AW296545	6703181	UI-H-BW0-aiq-b-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730621 /clone_end=3'	-1	AGGCATCTTGAAGTTCATAAAGAC AGAAGTAAGGGTCATTGAGTCATT
5830	db mining	Hs.255561	AW296567	6703203	UI-H-BW0-aiq-f-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730751 /clone_end=3'	-1	AGCTAAAGCCACGGAACTCAATGAGA TTTATGCATGGAAGGAAACAGGTT
5831	db mining	Hs.255569	AW296695	6703331	UI-H-BW0-abx-c-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730635 /clone_end=3'	-1	TGTTCTCTCTCGAACTCTGGAGCACA TCAGCTCTCTGCTGATAAACTGTT
5832	db mining	Hs.255572	AW296727	6703363	UI-H-BW0-abx-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730785 /clone_end=3'	-1	ATCTGGAGGATGGCAGTTTGAGAATT AGGACTAAGCCCGCTCCCCCTTTG
5833	Table 3A	Hs.255573	AW296730	6703366	UI-H-BW0-abx-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730791 /clone_end=3'	-1	CATTAGCTCTCTAAACATTGGCCTA AGGGATTGATAGGTGAAGCCTTTA
5834	db mining	Hs.255575	AW296758	6703394	UI-H-BW0-ajb-a-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730931 /clone_end=3'	-1	GGTAGGATTTATCCTTTTCTTCATGTG CAACTGTATAAACTGGCAAAGCA
5835	db mining	Hs.255577	AW296773	6703409	UI-H-BW0-ajb-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731015 /clone_end=3'	-1	AGTCTTATGGGACAGAGCAGCTCTCC AGTCTAGGATGGTAGAAGATTCTT
5836	Table 3A	Hs.255579	AW296797	6703433	UI-H-BW0-ajb-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731117 /clone_end=3'	-1	GAGTCTGTACCCCTTTCTAATAAACT GCTCTGGACACAATGAACCTGAA
5837	db mining	Hs.255580	AW296802	6703438	UI-H-BW0-ajb-f-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731155 /clone_end=3'	-1	CCATCGGGCAAGCCTTGGTGGGTTTCAT ATTCAGTGGCATTAGGGATTAAGG
5838	db mining	Hs.255590	AW296914	6703550	UI-H-BW0-ajc-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731294 /clone_end=3'	-1	CCATTTCTTCTGGATCCTCTCCTAGTT GTCTTTGTGTGGACGCACAAGCG
5839	db mining	Hs.255591	AW296947	6703583	UI-H-BW0-ajc-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731472 /clone_end=3'	-1	GATCCTTTGCTGACACTGGTTTCTCT CTTATTTTGGCCCGCCAATAAAAA
5840	db mining	Hs.255598	AW297024	6703680	UI-H-BW0-ajf-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731495 /clone_end=3'	-1	TCTGTCTGAAACTTCTTTTCTCTCTGA GAATTAATTTTCCAATGGACCGT
5841	db mining	Hs.255600	AW297026	6703662	UI-H-BW0-ajf-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731499 /clone_end=3'	-1	GATCTGTGTTTTCCTCCCAAAAGAG ATCATCTTCCAGAAAAAGAGGAT
5842	db mining	Hs.255601	AW297030	6703666	UI-H-BW0-ajf-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731507 /clone_end=3'	-1	TTCCATATGTCACTGTATCTGCCTGG CATTACCCCTTCTTAAACACACA
5843	db mining	Hs.288403	AW297036	6703672	AV757131 cDNA, 5' end /clone=BMFAKG04 /clone_end=5'	-1	GCTCACTACCACTTCTTCAAATCCAG CTAAAGCATCACGGCTCAATGA
5844	db mining	Hs.255614	AW297162	6703808	HNC68-1-F10.R cDNA	-1	GTCTGGTTGTTAGCTTCCCGATCCT CCACACATTGGAACCTAAGCATA
5845	db mining	Hs.255615	AW297175	6703811	UI-H-BW0-ajd-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731375 /clone_end=3'	-1	GGGCAATGGAGCCACAGACTCTCTA ACTTCAAGAGGTGTTTCATAGGTGT
5846	db mining	Hs.255618	AW297199	6703835	UI-H-BW0-ajd-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731477 /clone_end=3'	-1	AGCTGAGGTCAGACAAACCACAACAT ATATGCAGATTATCAGCAATAAA
5847	db mining	Hs.255617	AW297201	6703837	7k38c02.x1 cDNA, 3' end /clone=IMAGE:3477507 /clone_end=3'	-1	CCTGCCAGGGTTGTTCCGGAAGTCGC AGGTCGAAAAATCTCCTCCGCATAC
5848	db mining	Hs.255621	AW297220	6703856	UI-H-BW0-ajd-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731577 /clone_end=3'	-1	CTTCTCTGAAATGGTACGCCCTATACT TGCATTCTGAGAAGCCAAACAA
5849	db mining	Hs.255622	AW297233	6703869	UI-H-BW0-aji-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731684 /clone_end=3'	-1	AGTTTTCTGGCTAAGTCACCTCTTAA GGAGATCCCTGTAAAAATGACCCCT
5850	db mining	NA	AW297255	6703891	UI-H-BW0-aji-c-04-0-UI.s1 NCI_CGAP_Sub8 cDNA clone IMAGE:2731782 3', mRNA sequence	-1	CAGATTAAAAACCCATCCCGGCCCT CACCAGGTGTTACAACCTCTGTCC
5851	db mining	Hs.48820	AW297262	6703898	TAFII105 mRNA, partial /cds=(0,2405)	-1	AGCAAATACTCTGCCTGGAAATAAA ATTCTGTCACTTCAAGCATCTCCT
5852	db mining	Hs.255626	AW297265	6703901	UI-H-BW0-aji-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731826 /clone_end=3'	-1	TCCAGGCACTGTATAGGTGGCGAGG ACACAATGATAGGCAAGTAGTACA

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5853	db mining	Hs.255630	AW297294	6703930	UI-H-BW0-aj-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731938 /clone_end=3'	-1	ACAGACCCAAACCTCACAGAGTGAAA GGGGACTTTCTCACAGAGTGAAA
5854	db mining	Hs.255632	AW297313	6703949	7k46h07.x1 cDNA, 3' end /clone=IMAGE:3478525 /clone_end=3'	-1	TTGCTTCAGACTTTTAAACAACATCCT AGAAGCCAGAAACAATGAAGAAA
5855	db mining	Hs.255633	AW297317	6703953	UI-H-BW0-aj-h-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732038 /clone_end=3'	-1	TTCTGTCCAGGGCTTCAAAAGAGACTT CCATAGTTTTGGGAAGTGGAGTCA
5856	db mining	Hs.255634	AW297318	6703954	UI-H-BW0-air-a-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730121 /clone_end=3'	-1	GATATATTGAAGTCCAGAGGCAGAGC TAAACAGGTGATGCCACTGGGTCT
5857	db mining	Hs.255635	AW297328	6703964	UI-H-BW0-air-a-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730141 /clone_end=3'	-1	AGGCTCTTGTGAGTATTCCTTTGATT CCTGCTTCTGTCTTTTAAATCA
5858	Table 3A	Hs.255637	AW297339	6703975	UI-H-BW0-air-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730221 /clone_end=3'	-1	ACACACCAAAGAAATAGAAGAGTCT TTTTCTGCCCTTGGGAATCTGCA
5859	db mining	NA	AW297356	6703992	UI-H-BW0-air-d-08-0-UI.s1 NCI CGAP_Sub6 cDNA clone IMAGE:2730279 3', mRNA sequence	-1	ACACCCAGCACCACAGGGAAGAAA TAATTCACAGAGCTAAGTATTCCA
5860	db mining	Hs.330185	AW297367	6704003	UI-H-BW0-air-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730361 /clone_end=3'	-1	TGTGCCTGTGTGCTCCAGCCTCTTCC TATGTGTGTAACCTCAATAAACC
5861	db mining	Hs.255644	AW297374	6704010	UI-H-BW0-air-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730375 /clone_end=3'	-1	ACCGAGTGTACCAGAGAGGTGTAA AAATCCAGGTCATGTTTGACAC
5862	db mining	Hs.255645	AW297384	6704020	UI-H-BW0-air-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730423 /clone_end=3'	-1	TCCTGATTCCTCAAAGTACCCCTTCC CTACAACCTCTAATCATGCTTTGCT
5863	db mining	Hs.255646	AW297390	6704026	UI-H-BW0-air-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730465 /clone_end=3'	-1	CCATGATTTTTCCAATGGACAAGCAC TATTAACATGGGACTGTATTTCT
5864	Table 3A	Hs.255647	AW297400	6704036	UI-H-BW0-ais-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730152 /clone_end=3'	-1	AATAGAACTGATAGCCCATGATGATT GGCTGGCAGGGTTAAGGAAGTGGG
5865	db mining	Hs.255648	AW297401	6704037	UI-H-BW0-ais-a-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730154 /clone_end=3'	-1	TCCCAGGAGAGTCACATTTCTTTTTC ACTAAATAAGGAGGGGAAGAAAA
5866	db mining	Hs.255649	AW297407	6704043	UI-H-BW0-ais-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730194 /clone_end=3'	-1	GGGTTACCTCACTTTCTAGGTTCCCA AGATTCCCAAGTTAAGGAAGCTTT
5867	db mining	Hs.255650	AW297411	6704047	UI-H-BW0-ais-b-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730204 /clone_end=3'	-1	AAAGCGTCCAGTCCCTTAACCTCAA CACAGAAACATAACAATTTAGAA
5868	db mining	Hs.255653	AW297426	6704062	UI-H-BW0-ais-c-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730262 /clone_end=3'	-1	CCCAGGGCTCCTCCACCTGAAAGAAT TGTCAGGGTTTCAGATCAGCTAAA
5869	db mining	Hs.255657	AW297443	6704079	UI-H-BW0-ais-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730352 /clone_end=3'	-1	TGGCCTCCACCCATTAACTGTCTTT GCCTAAGACAAATAATCCAGGA
5870	Table 3A	Hs.255661	AW297522	6704158	UI-H-BW0-aja-e-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731106 /clone_end=3'	-1	TGTACTCTGATGCCTGAAAACTGTT AAGTGAAGACTTATCACATTACCG
5871	db mining	Hs.255665	AW297581	6704217	UI-H-BW0-ajg-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731718 /clone_end=3'	-1	ATCCTTCAGATTGAGCTGGGTGTGAG CATTCATTCCACAAGGCTACCTG
5872	db mining	Hs.255666	AW297590	6704226	RST6539 cDNA	-1	TGGATAAGCAATATGTTGGACTAGTA TGAAAAATGGCATTCCAGCAGTGA
5873	db mining	Hs.255672	AW297626	6704262	UI-H-BW0-ajg-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731918 /clone_end=3'	-1	TCCTAGCAGAAATATAGTGGGCATGA CCAGTATCCTAGTAGAGCTGACCC
5874	db mining	Hs.255673	AW297636	6704272	UI-H-BW0-ajg-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731996 /clone_end=3'	-1	AGTTTCTTCTTACAATGGGGTCTG AAATCCAGGGTTCCACACCAGGG
5875	db mining	Hs.255674	AW297649	6704285	UI-H-BW0-ajh-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731665 /clone_end=3'	-1	CCAAATACTTAGTGTAGTTGACTTGT CTTGGGTTGCACTGTAAGGCAGAG
5876	db mining	Hs.255675	AW297651	6704287	UI-H-BW0-ajh-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731689 /clone_end=3'	-1	CAAGAGTTTCCATGCGTCCAGTGATG ACCGGAATTAATCATGTATGGTGT
5877	db mining	Hs.255677	AW297664	6704300	UI-H-BW0-ajh-b-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731725 /clone_end=3'	-1	GTTTCTAACCCATAAGTGCTCATAC ATACATTGCTAGTCTAAAGAGCTTT
5878	db mining	Hs.255679	AW297692	6704328	UI-H-BW0-ajh-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731857 /clone_end=3'	-1	ACCGGCTAATTTTGAAGTGGCTTGT TTGTAAAAATAATCCTTCTGTGT
5879	db mining	Hs.255681	AW297694	6704330	UI-H-BW0-ajh-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731861 /clone_end=3'	-1	TGGTGGGACTATGTGTTATTTCTGTA TACTTGCAAGTGGGTAGATGTCACT

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5880	db mining	Hs.255682	AW297698	6704334	UI-H-BW0-ajh-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731859 /clone_end=3'	-1	ACTTCCTACCTCACAGGTTAGGATT CAAAGTGTGATTCCCCATTGTG
5881	db mining	Hs.255686	AW297728	6704364	UI-H-BW0-aly-a-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730888 /clone_end=3'	-1	GGGTGCTTTACAGGATTCTTGAAAT GTGTAGTGGATGCTGGCTCTAGGG
5882	db mining	Hs.255688	AW297749	6704385	UI-H-BW0-aly-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730988 /clone_end=3'	-1	ACAGAAGCAGGGGGTGCAGAAAGTTT CATAAAGGAGGTGCTTGGAAACAA
5883	db mining	Hs.342530	AW297756	6704392	UI-H-BW0-aly-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731032 /clone_end=3'	-1	CTATTGTGTGGGTGCGCTTGCTCTAC TCAACTTCAAATATTACACACCCC
5884	db mining	Hs.255691	AW297780	6704418	UI-H-BW0-aly-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731100 /clone_end=3'	-1	CAGGTGTGCTTACTGGCAGGAACCG AGGGAATAAATAAGATCACTGGAA
5885	db mining	Hs.255692	AW297781	6704417	UI-H-BW0-aly-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731102 /clone_end=3'	-1	ACCAGCCTTATGTGTGTGGGTATTCA ATACTCTGCACATTATATACTGTA
5886	db mining	Hs.255693	AW297785	6704421	UI-H-BW0-aly-f-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731134 /clone_end=3'	-1	GGGCATTGTGTACCCCTCTCACCA CCATCCCCATTAAAGCTTCGGGG
5887	Table 3A	Hs.255695	AW297813	6704438	UI-H-BW0-aly-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731192 /clone_end=3'	-1	CTGTATCTACAACCTCTGACTTCAGA TTTTTGCTTTCTTCAAACAGCCT
5888	Table 3A	Hs.255697	AW297827	6704452	UI-H-BW0-aly-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731244 /clone_end=3'	-1	AGCAAGACTTAACCACTAATTACTATT ATCTGACCCAGGAAACTCCGCC
5889	db mining	Hs.255698	AW297843	6704468	UI-H-BW1-aaa-c-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083913 /clone_end=3'	-1	TGGATAGTTGCTCAATGTAGCAGTGA TGTTCTTGAATTGCCAGCAGAGC
5890	db mining	Hs.328317	AW297929	6704585	yg18e06.s1 cDNA, 3' end /clone=IMAGE:32551 /clone_end=3'	-1	CCAACAGATTCTGCTTACCCTGAGG TGAAAGCCTCGTTTGAGAACCAAAT
5891	db mining	Hs.255705	AW297949	6704585	UI-H-BW0-ajn-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732229 /clone_end=3'	-1	CAACCTTCTTGTGAATTGATTACTA CTCATCAGGGTCATGCACAAGCA
5892	db mining	Hs.255706	AW297951	6704587	UI-H-BW0-ajn-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732257 /clone_end=3'	-1	ACATTCAAACCTGCCAGAATATGACTG TAAACAGCGAAGTGTTCTCTTGC
5893	db mining	Hs.255708	AW297970	6704606	UI-H-BW0-ajn-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732323 /clone_end=3'	-1	TCTTCCTGGGAATGTGATGTGTTTT CACTGGTTCTAATTCTGTCTTCT
5894	db mining	Hs.255710	AW297974	6704610	UI-H-BW0-ajn-g-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732355 /clone_end=3'	-1	ACTTATTAATCTCACCTCAGCCTCA GGGATGTATGTAGGGAAGGAGCAT
5895	db mining	Hs.255713	AW297994	6704630	UI-H-BW0-ajn-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732421 /clone_end=3'	-1	ACATTCTGTCTATTAGTGAATAAGAA GCTGAGGTGTGACTAAGAAGACAA
5896	db mining	Hs.255717	AW298042	6704678	UI-H-BW0-ajp-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732629 /clone_end=3'	-1	CCTCCTTGATAAAATCAAGAACAGGT TAGATTAAGCAGTAAATCCTAGACT
5897	db mining	Hs.330189	AW298048	6704684	UI-H-BW0-ajp-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732665 /clone_end=3'	-1	TCCTGGCCTTTGTGGGTTTTTAATTC CCTTTACCTTTTCCCTTTTGGAT
5898	db mining	Hs.255721	AW298073	6704709	UI-H-BW0-ajp-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732769 /clone_end=3'	-1	ACTGTGCAACTACAATTCTCAGATA GTCCCATTTGTTAAATCACGCAT
5899	db mining	Hs.342533	AW298095	6704731	UI-H-BW0-ajs-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732878 /clone_end=3'	-1	CCTTCCTCTTGCCTGTAGGTTCTGT GGCTATAACAAATCATACTTTT
5900	db mining	Hs.255725	AW298108	6704742	UI-H-BW0-ajs-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732916 /clone_end=3'	-1	TAAATGCTTCCCTGGCTCTCCCTGG GTTTCAGTTTCTATCCATGCCCTG
5901	db mining	Hs.255726	AW298110	6704746	UI-H-BW0-ajs-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732924 /clone_end=3'	-1	TGTTCTCCTCCCAAGTCTCTGGTTC TATTTGGCTTTTTCAGCTCTGTGC
5902	db mining	Hs.255727	AW298123	6704759	UI-H-BW0-ajs-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733000 /clone_end=3'	-1	GCATTTCAGGGACACAAATGGTCCAT GGCAGAGACCAGTAATGCCAGATA
5903	db mining	Hs.255736	AW298201	6704837	UI-H-BW0-ajt-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732987 /clone_end=3'	-1	TTTTATCCCCGCTTTAACTTTGTTGC TTGGTACTTTTCTGTGGTTACA
5904	db mining	NA	AW298208	6704844	UI-H-BW0-ajt-e-05-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2733009 3', mRNA sequence	-1	CACGCACCCAACTCCCCACTGCTCCT CTCCATCCAGATGTTCTGTCCAGAG
5905	db mining	Hs.255740	AW298234	6704870	UI-H-BW0-ajt-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733113 /clone_end=3'	-1	TTTGAGGGCAATTTAATGGTTAAGTG TAGGAAAAATCCACTCTTACAGTGT
5906	db mining	Hs.330191	AW298238	6704874	UI-H-BW0-ajt-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733151 /clone_end=3'	-1	GGCCTTTTGATTTCCATTGGGGTCC CCCGCTTCCCATTTTGGTTTTT

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5907	db mining	Hs.255743	AW298239	6704875	UI-H-BW0-ajl-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733153 /clone_end=3'	-1	GACAGTTTGGGGAAGGATTGAAGG TCTGCGTCAAGAGAACAGAAAACC
5908	db mining	NA	AW298271	6704994	UI-H-BW0-ajk-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732184 /clone_end=3'	-1	AGGGGCGCTTTTACCGGTTTGTTCCT CTTAAATTTTAAAGGAATTGAATT
5909	db mining	Hs.183669	AW298312	6705035	mRNA for KIAA1271 protein, partial cds /cds=(72,1700)	-1	TCCTCTTCTTGTCACTGTGAAGCGA TGAATAAACCTGGGTGTAGATCCA
5910	db mining	Hs.302681	AW298348	6704908	7j80e10.x1 cDNA, 3' end /clone=IMAGE:3392778 /clone_end=3'	-1	CCTAGAAATTATTATACAGGGATAAAT GAGGCACTGAAGTGGGAGAACC
5911	db mining	Hs.255746	AW298349	6704909	UI-H-BW0-ajl-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731795 /clone_end=3'	-1	ACGACAACTGCACAGTAAATATCAC AAACACGGAAATACCAGTGTCT
5912	db mining	Hs.255747	AW298355	6704915	UI-H-BW0-ajl-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731835 /clone_end=3'	-1	ACCATGACTTGGCAAAGAGTTTCAAG AGAGGGCATAATCAAAGTAACCA
5913	db mining	Hs.255749	AW298388	6704948	UI-H-BW0-ajl-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731983 /clone_end=3'	-1	GATTAATCAAGGGAAGAGCTTCAAGC AGAGCTCCTTAGGTTTTTCAAAA
5914	Table 3A	Hs.313413	AW298430	6705066	602721745F1 cDNA, 5' end /clone=IMAGE:4838506 /clone_end=5'	-1	GCTCAGGGGACAGCTATTCTTTTCA AAGCGTTTACCGACTGGATCACCT
5915	db mining	Hs.255762	AW298437	6705073	UI-H-BW0-ajl-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732199 /clone_end=3'	-1	TGAGAGCTTCTCTCTCTACGATC CAACCATGTCAAACATTTCTACA
5916	db mining	Hs.255763	AW298445	6705081	UI-H-BW0-ajl-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732245 /clone_end=3'	-1	TGTGCCAACGCATGATTCTTTGAGT AAATTTCTAAACGTCACAGAAGTT
5917	db mining	Hs.255764	AW298447	6705083	UI-H-BW0-ajl-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732249 /clone_end=3'	-1	AGTCAACATGGAGCAAGTGAGCTAAG GAAGTAATGGAAGCTTTTGAGA
5918	db mining	Hs.255766	AW298482	6705118	UI-H-BW0-ajl-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732397 /clone_end=3'	-1	AGCTCAGGTCTTCCCTCATCTGTTAG TTTCTGGAGTCTGTTCTCATACT
5919	db mining	Hs.255767	AW298489	6705125	UI-H-BW0-ajm-a-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732078 /clone_end=3'	-1	AAACATACTCTCTTACCAGCACTC AGACATTTGTATCCAGAGAAAGCT
5920	db mining	Hs.255768	AW298490	6705126	UI-H-BW0-ajm-a-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732080 /clone_end=3'	-1	AGTCTGTCAATTGTTTAAAGCCTGTGA TCTTTCTTTTCCAGTTAAGAGTT
5921	db mining	Hs.255769	AW298494	6705130	UI-H-BW0-ajm-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732112 /clone_end=3'	-1	TGTCCTCTCAACCCTACTTGTGGTTT TACACTGTTAATTACACTATTTGC
5922	db mining	Hs.132781	AW298502	6705138	class I cytokine receptor (WSX-1), mRNA /cds=(138,2048)	-1	GTGTGTGTATGTTTGTGGGCGTAG GACAGGTTTCGGGGATGCGCGGTAC
5923	db mining	Hs.255770	AW298503	6705139	UI-H-BW0-ajm-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732134 /clone_end=3'	-1	CTGTGCTTGACTATTGAAAACCTTGA ATTGGGATGCCAAAGTTACTTCCT
5924	db mining	Hs.255772	AW298510	6705146	UI-H-BW0-ajm-c-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732180 /clone_end=3'	-1	GGTTGTATCAAAAGAACTCCACATCC ATATTGAATAAACTCCCACTAGCC
5925	db mining	Hs.255777	AW298559	6705195	UI-H-BW0-ajm-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732408 /clone_end=3'	-1	GGCTGCCAGATCTCGTGGGAAGAA GACCACAGGAGGACTCGGCTCAATG
5926	db mining	Hs.255779	AW298607	6705243	UI-H-BW0-ajr-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732615 /clone_end=3'	-1	TGGAAAAATGATAGCAGCCAACTTGA CAGAGAACCACAGCATACACATTC
5927	db mining	Hs.255782	AW298616	6705252	UI-H-BW0-ajr-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732659 /clone_end=3'	-1	TTGGTTTTGGGGATTGGGAAGTCTTA AGCCAAATTGTCCCGGTCTCCCC
5928	db mining	Hs.255783	AW298627	6705263	UI-H-BW0-ajr-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732707 /clone_end=3'	-1	GCCCTATATCTAGTGAGCAGGTTGTG GCAATCAGGAAGGGATTGATATT
5929	db mining	Hs.255784	AW298632	6705268	UI-H-BW0-ajr-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732743 /clone_end=3'	-1	TGCACGCAATGCTTGAAGTGTCCCA GGTATTTAGTTTCAGTAAATTTT
5930	db mining	Hs.255785	AW298647	6705283	UI-H-BW0-ajr-h-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732801 /clone_end=3'	-1	CTGTAGGTATGAGCTGCCAGGATCCA GGTGTGACTCGGGTATTCTAGGG
5931	db mining	Hs.255788	AW298675	6705311	UI-H-BW0-ajr-o-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732524 /clone_end=3'	-1	TCCCATTTGGGGGGTGGGCTGTTTAA ATTTTGACTCCCTGTTTTAAACCC
5932	db mining	Hs.255794	AW298720	6705356	UI-H-BW0-ajr-g-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732724 /clone_end=3'	-1	CCACTTGCATCTCTTCTGGGGGTCTT TTCCTTTCTTCTGTTCTAAGGC
5933	db mining	Hs.255797	AW298752	6705388	UI-H-BW0-ajr-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732506 /clone_end=3'	-1	TGGGTAATCAACACTCAACCATCAAC AAACACTCTCTATTCCAGGCACTG
5934	db mining	Hs.255799	AW298806	6705442	RC4-MT0235-061200-011-e11 cDNA	-1	AGGAGAAATAATTAGAGTGGCACACT AGCATGATGGTAAACATTTCTGTCA

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5935	Table 3A	Hs.157396	AW300500	6710177	xs66c06.x1 cDNA, 3' end /clone=IMAGE:2774602 /clone_end=3'	-1	AGGAGTTCAGAAAGCAGAGATTTCCA GGTCCATGCACCAAGCTCATGTG
5936	Table 3A	Hs.262789	AW300868	6710545	xk07d09.x1 cDNA, 3' end /clone=IMAGE:2666033 /clone_end=3'	-1	CTTGTCTCTCTGATCCAGGGCTCC AGTGCCCATGTCCAGTGCCCTTGGT
5937	db mining	Hs.255880	AW337887	6834513	he12d07.x1 cDNA, 3' end /clone=IMAGE:2918797 /clone_end=3'	-1	GCATCTCCCCGCTGTGACGCTCAGC CCTCTCCTACCAAAATCTCTTTTGA
5938	Table 3A	Hs.328348	AW338115	6834741	tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3'	-1	GGCGTTTCCCATTTGACCAGTTTGACC CTGGTTTGAATAAGAGAAGTGCG
5939	db mining	Hs.255920	AW339530	6836156	he13d09.x1 cDNA, 3' end /clone=IMAGE:2918897 /clone_end=3'	-1	AGCCCATTTGAAACCTTTGGCAAAATG TCAGACCTTAAGACTTTCCACTAT
5940	Table 3A	Hs.255927	AW339651	6836277	he15g04.x1 cDNA, 3' end /clone=IMAGE:2919126 /clone_end=3'	-1	TCAGAGACAACGGAAGCTGAAAAATA AGAGCTGAGAAAGGAAGAACTTTT
5941	Table 3A	Hs.207995	AW340421	6837047	hc96h02.x1 cDNA, 3' end /clone=IMAGE:2907891 /clone_end=3'	-1	ATATACATACAAATCTAAGCTCCAAG AAGCCTAAGAAAACCCCTTAGGGG
5942	Table 3A	Hs.256031	AW341086	6837631	xz92h04.x1 cDNA, 3' end /clone=IMAGE:2871703 /clone_end=3'	-1	GGGCAATTATCATCGGGACTCGTTTC ATCTCTAGACCTTCACCTACCTGA
5943	Table 3A	Hs.283667	AW341449	6838075	arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA /cds=(9,1982)	-1	AGCTCTGGAGTGCCCTCCCTCCAAA TAAAGTATTTAAGCGAAGCACTGA
5944	Table 3A	Hs.337988	AW440517	6975823	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGCTCTTCATTAAGCAAACTA
5945	db mining	Hs.256956	AW440813	6976044	he03b05.x1 cDNA, 3' end /clone=IMAGE:2917905 /clone_end=3'	-1	CCCTCAGGCATAGAAATTGAATCTGA AATGGCTGATGAATAAGCAAAAGGC
5946	db mining	Hs.313573	AW440817	6976048	he03c02.x1 cDNA, 3' end /clone=IMAGE:2917922 /clone_end=3'	-1	CAGCCCTGCCTGAGTTTTTGACACCT GCATCCCTCCCTGCCTCACCTCAC
5947	Table 3A	Hs.256961	AW440866	6976172	he05f02.x1 cDNA, 3' end /clone=IMAGE:2918139 /clone_end=3'	-1	AGAGCAGGAGAAATCCTACTGCATTA TTAATCTGAAAGCACAAAGGACAGC
5948	Table 3A	Hs.173730	AW440869	6976175	Mediterranean fever (MEFV), mRNA /cds=(41,2386)	-1	CTGTCTTGGTTTGTATGGGAAATCT GCGGGTTGTGGAATATTAGGTTCT
5949	Table 3A	Hs.118446	AW440965	6976271	HNC35-1-D12.R cDNA	-1	TGGGATTATAGGGGGAGACAGGAGT TGTGGAATTACAGGAGAGGTTCACT
5950	db mining	Hs.118446	AW440965	6976271	HNC35-1-D12.R cDNA	-1	TGGGATTATAGGGGGAGACAGGAGT TGTGGAATTACAGGAGAGGTTCACT
5951	Table 3A	Hs.256971	AW440974	6976280	he08e12.x1 cDNA, 3' end /clone=IMAGE:2918254 /clone_end=3'	-1	CTGAGAAAAGGAGTGTCTCTCTCTG CTCCAACTTCCAGTAGCTTCCA
5952	Table 3A	Hs.342632	AW444482	6986244	UI-H-BI3-akt-e-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2739777 /clone_end=3'	-1	TCGAGGTTCTTCCCAAGAAAGCCCA ATCTTATAAAGTGTACTTCCCT
5953	Table 3A	Hs.250	AW444632	6986394	xanthine dehydrogenase (XDH), mRNA /cds=(81,4082)	-1	TGCAATGAGGCAGTGGGGTAAGGTT AAATCCTCTAACCGTCTTTGAATCA
5954	Table 3A	Hs.335815	AW444812	6986574	UI-H-BI3-ajy-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3'	-1	TGGCAACTCAACTCCTTGATGGCGA TAATCTCTGGTATGAATATGAGCC
5955	Table 3A	Hs.99665	AW444899	6986661	UI-H-BI3-ajz-d-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733373 /clone_end=3'	-1	TTGTGCTCCTGATACGACGTTGCCAC AGTTAATCCGTTCTGATCTCTGCT
5956	Table 3A	Hs.257283	AW450350	6991126	UI-H-BI3-akn-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2734825 /clone_end=3'	-1	CAAGCCTAACTTTCCAACACTCCCGC GACGCAACCCCTTCCCTTTCTCTC
5957	Table 3A	Hs.313715	AW450835	6991611	UI-H-BI3-alf-f-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2736539 /clone_end=3'	-1	CACGGTTAGAGTACCAAACTGTAT TTCAGGGGACATCTTCCAGCTCC
5958	Table 3A	Hs.199014	AW450874	6991650	601499703F1 cDNA, 5' end /clone=IMAGE:3901440 /clone_end=5'	-1	CCAAAGGCTCACTACCCCTGTGCGTT GTCCAGCACACAGACACTATGTGC
5959	Table 3A	Hs.342873	AW451293	6992069	RC3-HT0230-130100-014-g06 cDNA	-1	TGCTTGGGAAATTTGGTTTGTAAACC TAAATAGCCCTTATTTCTGGGGA
5960	Table 3A	Hs.101370	AW452023	6992799	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	CATCTGCTGAGCAGTGTGCTGTGTCA ACCTCCTCTAGGTCTCCTCTATG
5961	Table 3A	Hs.342735	AW452096	6992953	UI-H-BI3-alo-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3'	-1	CTTTCTGCCTGAAGCTGCCCCCATGA CTCCCTTCTTTGTGCAAAAGCATG
5962	Table 3A	NA	AW452467	6993243	UI-H-BI3-als-e-09-0-UI.s1 NCL CGAP_Sub5 cDNA clone IMAGE:3088832 3', mRNA sequence	-1	GAAATGAGTTGGTGTCTTACAGAAT GAGGATCCCCAGAGCCATCTTGCC
5963	Table 3A	Hs.257579	AW452513	6993289	UI-H-BW1-ame-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069628 /clone_end=3'	-1	GTCTCCCTCCCACTCTCTGCCTTACC TGGTATCTATGACTCGACTGAAAT

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5964	db mining	Hs.257581	AW452528	6993304	UI-H-BW1-ame-c-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069684 /clone_end=3'	-1	TGCGAGAGGAAGCAGAGACCACCTT GAAACTCGGGTGCAATTAAGTCCTTG
5965	db mining	Hs.257582	AW452545	6993321	UI-H-BW1-ame-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069742 /clone_end=3'	-1	TTAGCCACTGCTATTCTAGGTTCCCTT GATGGAGCCCCACTCCCACGCCTA
5966	db mining	Hs.257630	AW452932	6993708	UI-H-BW1-ame-d-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069325 /clone_end=3'	-1	ACCACCCAGAGGTTGCTGGCTTCCTT AATAAAGCTAACTTTCCTTTCACC
5967	db mining	Hs.257632	AW452953	6993729	UI-H-BW1-ame-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069415 /clone_end=3'	-1	AGGGGAGCCAGTGTTTGGTGCAT GGGAAGTGTTCTCATAAAATTCATT
5968	db mining	Hs.257633	AW452960	6993736	UI-H-BW1-ame-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069429 /clone_end=3'	-1	GCACCAGACTTCTGAACAGGCTGGG AGAGTGAGGCATAAACACATGAAAT
5969	db mining	Hs.257636	AW452985	6993761	UI-H-BW1-ame-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069527 /clone_end=3'	-1	ACACAGTACTTGTGAGATGTTGGC TTCTTGGTTATGGCATGAATTCT
5970	Table 3A	Hs.257640	AW453021	6993797	UI-H-BW1-ame-c-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069290 /clone_end=3'	-1	ACTTATCTTTGCCACCCATGTTCCCT GGATGCCTTGCCCTCCTCTTTCAT
5971	db mining	Hs.257644	AW453034	6993810	UI-H-BW1-ame-d-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069340 /clone_end=3'	-1	AAACAGGAAGCCTCTCATGAATTTGA CCAAGGAGCTACATTCGTTCTCTA
5972	db mining	Hs.257645	AW453039	6993815	UI-H-BW1-ame-d-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069350 /clone_end=3'	-1	TGAGGAAGAGGAGATTTATTAAGCCC CTTCTTTTAGGCTAGGAGGTTTCC
5973	Table 3A	Hs.257646	AW453044	6993820	UI-H-BW1-ame-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069384 /clone_end=3'	-1	GGACACTGGCTTTTGTGCAGCTCTTC ATCACAGAGTCTGTTGAGCTACAA
5974	db mining	Hs.257647	AW453055	6993831	UI-H-BW1-ame-c-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069406 /clone_end=3'	-1	ACAGTGATTTTCAACCAAGGGGCTTT TTCAAACATACATTCCTTAGCTCCC
5975	Table 3A	Hs.257667	AW467193	7037299	he07a04.x1 cDNA, 3' end /clone=IMAGE:2918286 /clone_end=3'	-1	GGTGGTGGCTACAAGGGTGATTGCC TTATGATAATTGACCGTGTCATAAT
5976	db mining	Hs.257668	AW467208	7037314	he07c09.x1 cDNA, 3' end /clone=IMAGE:2918320 /clone_end=3'	-1	AGCTGGGAGGCCATTACTTTTGTCT GAGTCTTCTGGAGTTCTAGCAAAA
5977	db mining	Hs.255877	AW467312	7037418	he09b01.x1 cDNA, 3' end /clone=IMAGE:2918473 /clone_end=3'	-1	AGTTGCATTAACCTGAGCTTAGATGT GTAAGTTTGCTAACGGATGGGTTT
5978	db mining	Hs.257677	AW467338	7037444	he09e07.x1 cDNA, 3' end /clone=IMAGE:2918532 /clone_end=3'	-1	CCTCTAAGGCATTTATTTACTGACAA CATAAAATCTTGAACCCAGGTCA
5979	db mining	Hs.257678	AW467385	7037491	he10d12.x1 cDNA, 3' end /clone=IMAGE:2918615 /clone_end=3'	-1	TCACCTCCATCAACTTACTAGCACAT AAAGGGTGGGATTTTCATGTGTGA
5980	Table 3A	Hs.257680	AW467400	7037506	he10f11.x1 cDNA, 3' end /clone=IMAGE:2918637 /clone_end=3'	-1	CTGGCAAGGCATGGGTACAACCTG CTCTGTGATCTACCTTCTGAACCAC
5981	db mining	NA	AW467421	7037527	he17b02.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919243 3' similar to contains Alu repetitive element; con	-1	ACACCTGTGGTATATTTGTATCATTC GTCTGGTTTCTCACCCTTCTCTAA
5982	Table 3A	NA	AW467437	7037543	he17d05.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919273 3', mRNA sequence	-1	AACCCTCGTAAGGTTTCATCTTCCCTT GATTGCAAAATGAGTTTGTGTGAA
5983	db mining	NA	AW467445	7037551	he17e08.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919302 3' similar to contains element MSR1 repetitive el	-1	CCCCTTCACCTTCCTTAATAACTC GTTTGCAGGCTAATTCATCAAAT
5984	db mining	NA	AW467448	7037554	he17f02.x1 NCL_CGAP_CML1 cDNA clone IMAGE:2919291 3' similar to contains Alu repetitive element; con	-1	ATTTTGCTCATTACCTGTCAGGAGAA AACCCTCCTCCCCAGTCTCCACT
5985	Table 3A	Hs.257687	AW467501	7037607	he19e06.x1 cDNA, 3' end /clone=IMAGE:2919490 /clone_end=3'	-1	ACCTACTGAATCTCCAGATTGCCAAG TGAAACACAATGGTTGCCTCTTCA
5986	db mining	Hs.257688	AW467571	7037677	he21f02.x1 cDNA, 3' end /clone=IMAGE:2919675 /clone_end=3'	-1	TGCGAAAGCTAATTCCTAGTATGAA TAAACTTCAGACCTTGCTCTCCTT
5987	db mining	Hs.257690	AW467582	7037688	602497524F1 cDNA, 5' end /clone=IMAGE:4611316 /clone_end=5'	-1	AGCCTGAGGTGGGTGAAGAAAATAC CTGCTTTATACTGTTCTGGAAACTC
5988	db mining	Hs.266387	AW467607	7037713	he22c05.x1 cDNA, 3' end /clone=IMAGE:2919752 /clone_end=3'	-1	CTTTTCCCCTTCATGGTAGTTGCTGC TTAAGTTTCTCTAACATGCCTGCA
5989	Table 3A	Hs.257695	AW467746	7037776	he23d05.x1 cDNA, 3' end /clone=IMAGE:2919849 /clone_end=3'	-1	TGAATGTGCAGATGCAGAACCCATTG ATATGGAGGGCTGAGTGTCTGAAA
5990	Table 3A	Hs.257705	AW467863	7037969	he27c04.x1 cDNA, 3' end /clone=IMAGE:2920230 /clone_end=3'	-1	TGTACTACTTATTTATGTGTAACCAT ACACAGGGCTAGAAAGGAAGGAT

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5991	Table 3A	Hs.257706	AW467864	7037970	he27c05.x1 cDNA, 3' end /clone=IMAGE:2920232 /clone_end=3'	-1	TGTAGAATTGCGGAGTAGAAAGACCC TTGAAAGATCATTTGTCTGTGGT
5992	Table 3A	Hs.257709	AW467992	7038098	he30b01.x1 cDNA, 3' end /clone=IMAGE:2920489 /clone_end=3'	-1	GCTCAAGTTCACGACCTGGGGAA TTCTAAGCCTGAGGAAGACAAGGTG
5993	db mining	Hs.257713	AW468139	7038245	he32g11.x1 cDNA, 3' end /clone=IMAGE:2920772 /clone_end=3'	-1	TGTTTTATGTCTGAGCAAGCAAATT GCTGCAATTAATACCAATTT
5994	Table 3A	Hs.257716	AW468207	7038313	he34a12.x1 cDNA, 3' end /clone=IMAGE:2920894 /clone_end=3'	-1	AGGCCTGATATTGAAAGCTTTTGATA CTGAGATCCTATTAATCTCAGATGA
5995	db mining	Hs.257719	AW468316	7038422	he36a05.x1 cDNA, 3' end /clone=IMAGE:2921072 /clone_end=3'	-1	TGTTAGTTTGTCTTTGAAATTTCTTGG AGGGTACTCTTCAGGGCTTCACA
5996	db mining	Hs.278060	AW468430	7038536	he37h10.x1 cDNA, 3' end /clone=IMAGE:2921251 /clone_end=3'	-1	TAGTGATTATCTCCAGGAATCAAGTA CAAACCTTTGAAAAAGACTGGAGGT
5997	Table 3A	Hs.257727	AW468431	7038537	he37h11.x1 cDNA, 3' end /clone=IMAGE:2921253 /clone_end=3'	-1	TTGTGCCCAAGGGCTCAGACTGAAAG AATGCAATGTGAGAGGTATGCCAC
5998	db mining	Hs.330268	AW468459	7038565	he38d05.x1 cDNA, 3' end /clone=IMAGE:2921289 /clone_end=3'	-1	TCTGTGAAATCTTTCTGCAATGTCT TTGCTTGTCTGACTCAGCTTTT
5999	db mining	Hs.257738	AW468559	7038665	he41a07.x1 cDNA, 3' end /clone=IMAGE:2921556 /clone_end=3'	-1	TGCTCTTAACGCACAGATGTTACTTC AGCACCACAAGGACTGTTGATGGA
6000	Table 3A	Hs.257743	AW468621	7038727	he42e03.x1 cDNA, 3' end /clone=IMAGE:2921692 /clone_end=3'	-1	CAGTCAGATGTTGGAATTGGGGGTA GAGGGATTATAGAGTTGTGTGTGCT
6001	Table 3A	Hs.122116	AW469546	7039652	hd19a09.x1 cDNA, 3' end /clone=IMAGE:2809992 /clone_end=3'	-1	AAAGGAGGGACTATGGCATCAAACA GCCTCTTCAGCACAGTGACACCATG
6002	Table 3A	Hs.80618	AW510795	7148873	hypothetical protein (FLJ20015), mRNA /cds=(31,522)	-1	ACCCAGTTTGTGCATAGTTCATGATC CTCTATAAAACCACTTTTGTGGA
6003	Table 3A	Hs.193669	AW512498	7150576	hypothetical protein DKFZp586J1119 (DKFZp586J1119), mRNA /cds=(27,2153)	-1	CTGTGGGCTCTGAAGCGAGCTGGT TTAGTTGTAGAAGATGCTCTGTTT
6004	Table 3A	Hs.42915	AW572538	7237271	ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258)	-1	TGGAATGGACTCTTAAACAATGAAA GAGCATTTATCGTTTGTCCCTTGA
6005	Table 3A	Hs.342858	AW572930	7237663	hf17f07.x1 cDNA, 3' end /clone=IMAGE:2932165 /clone_end=3'	-1	TCACTACCTCAATTGTTTACAAGGT GGATATGGGCAGGCAACAGATACT
6006	Table 3A	Hs.325981	AW573211	7237944	602679187F1 cDNA, 5' end /clone=IMAGE:4812093 /clone_end=5'	-1	CTAGGCCGGATGGGCCAGAGAAGGA GAACCATGGCAGGAGCCGGAAGCAG
6007	db mining	Hs.258933	AW589231	7276337	he27g09.x1 cDNA, 3' end /clone=IMAGE:2920288 /clone_end=3'	-1	AAATGTTGAGCAACTGTTCATAACA GCACATTTGTGTGTTCAATGGCT
6008	Table 3A	Hs.304925	AW592876	7280068	hg04d05.x1 cDNA, 3' end /clone=IMAGE:2944617 /clone_end=3'	-1	CTGGCACATCCAGGTTTTAGAGCAGG CAGCTGAGATTTCAAAATGAGG
6009	Table 3A	Hs.298654	AW614181	7319367	hg77d03.x1 cDNA, 3' end /clone=IMAGE:2951621 /clone_end=3'	-1	GGAGCGGAATACAGTAAAGCACTG GACTGACCTAAGAGTTGTTTCTGC
6010	Table 3A	Hs.259842	AW614193	7319379	cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145)	-1	ACACCATTTACGCGTTGGATCACAGA CAGCTCTTCTTTATATCCAGCA
6011	Table 3A	Hs.342967	AW629176	7375966	602618939F1 cDNA, 5' end /clone=IMAGE:4745649 /clone_end=5'	-1	CCACCTTGCTGCCTTTTGAACACTC AGGAAATATAGTTGGCTAAACTG
6012	Table 3A	Hs.140720	AW829485	7376275	FRAT2 mRNA, complete cds /cds=(129,830)	-1	CACTTCGCAACGGAGTGTTTGAAATT GTGGTGGTCTGATTATAGGATT
6013	db mining	Hs.175437	AW771958	7704007	hn66h09.x1 cDNA, 3' end /clone=IMAGE:3032897 /clone_end=3'	-1	GCTTTGGCAGATGGATTAACTTTGT CTTTTGAGCCAGATCAATATCTA
6014	Table 3A	Hs.151393	AW778854	7793457	glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005)	-1	AGAATGCCTGGTTTTCGTTTGCAATT TGCTTGTGTAATCAGTTGTAAA
6015	Table 3A	Hs.109441	AW780057	7794660	cDNA FLJ14235 fis, clone NT2RP4000167 /cds=(82,2172)	-1	TTCTGAACATTTTGTCAAGCTACAAC AGGTTTGGAAACCTCTGTGGGG
6016	Table 3A	Hs.343475	AW873028	8007081	601556208T1 cDNA, 3' end /clone=IMAGE:3826392 /clone_end=3'	-1	TGCAAGTGGATGGTTTGGTATCACTG TAAATAAAAGAGGGCCTGGGAAA
6017	Table 3A	Hs.166338	AW873324	8007377	hi92a07.x1 cDNA, 3' end /clone=IMAGE:3009396 /clone_end=3'	-1	GTGGCTTTTCTGTTGACGCCAAAGGT TACTCCCTCTGCCTCACCATAAAA

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6018	Table 3A	Hs.90960	AW873326	8007379	602563938F1 cDNA, 5' end /clone=IMAGE:4688769 /clone_end=5'	-1	ACCTCCTACGCTCTGTTTTCTGGCTGT GGTGACTTGGGATTTTAAACCTTA
6019	Table 3A	Hs.120243	BE044364	8361417	gamma-parvin (PARVG), mRNA /cds=(0,995)	-1	ATCGTTGGATTATCTTTGAACCCCT TGTTGGATCATTTTGAGCCGCCT
6020	db mining	Hs.157489	BE047166	8384219	602482536F1 cDNA, 5' end /clone=IMAGE:4575393 /clone_end=5'	-1	AGCTCCAAAGTGGTTTGATGACCACA GGCTAAAATTCATAGCTCTTAAAT
6021	Table 3A	Hs.82316	BE049439	8366494	interferon-induced, hepatitis C- associated microtubular aggregate protein (44kD) (MTAP44), mRNA /cds=(0,1334)	-1	TCAGAAAGGAGAAAACACAGACCAAA GAGAAGTATCTAAGACCAAGGGA
6022	Table 3A	Hs.121587	BE217848	8905166	602637362F1 cDNA, 5' end /clone=IMAGE:4765191 /clone_end=5'	-1	GCATCACGATTGTCTACATAAGTCC AGTTTCTCTCGCGTTTGTTTGGC
6023	Table 3A	Hs.5734	BE218938	8906256	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145)	-1	ATACAGGGTTCATCCAGAAGCATT CAGTCAGAGCAAGTTAAAGTCAGT
6024	Table 3A	Hs.203772	BE220869	8908187	F5HD region gene 1 (FRG1), mRNA /cds=(191,967)	-1	AAGTGCCAGATTTTGATAATCACCAG CCTCTCATTCACCTCTATGTTGC
6025	Table 3A	Hs.73931	BE220959	8908277	major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA /cds=(57,842)	-1	ACCCCTGGTCACTGGTGTTCACAA TTCTGGCAAGTCACATCAATCAAG
6026	Table 3A	Hs.128675	BE222032	8909271	hr61g11.x1 cDNA, 3' end /clone=IMAGE:3133028 /clone_end=3'	-1	AGCTCTGGAGCCTTTGCTTCTCTCAA TACGAGCGGGAAGCTGCGTTGAGCG
6027	Table 3A	Hs.167988	BE222301	8909619	neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747)	-1	AAGTTGTCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTTAGG
6028	Table 3A	Hs.79914	BE222392	8909710	lumican (LUM), mRNA /cds=(84,1100)	-1	ATTGACAGATGTCAGAAAGGAAGT TAGTGAGTCAAGACAAACACATCT
6029	Table 3A	Hs.89237	BE326857	9200833	hr61h06.x1 cDNA, 3' end /clone=IMAGE:3133403 /clone_end=3'	-1	CCCCTACCCTGGAAAGTAATATACT GAAGTCTCATCACTGTTTGGG
6030	Table 3A	Hs.83623	BE328818	9202594	nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318)	-1	TGTTTCGTAATTAATAGGCTTGGC CCAGAAGACCCACTCAATTGCCTT
6031	Table 3A	Hs.27774	BE348809	9260662	602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5'	-1	AGCTAGTGATGTTTGTCCAAAGGAA GATTCTGACAACAGCTTCAGCAGA
6032	Table 3A	NA	BE348955	9260808	hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence	-1	ACACAGACATATTGACCGCACACAAC ACTGAAATGGACTGACTTGAGAAA
6033	Table 3A	Hs.56156	BE349148	9261087	601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5'	-1	TGGTTCTCTGATTGTGAATGAGCACC TGGATATGTCAATTAATGCCCA
6034	Table 3A	Hs.315050	BE351010	9262791	ht22g04.x1 cDNA, 3' end /clone=IMAGE:3147510 /clone_end=3'	-1	GGTCCATGTCACCGTGAGTACACCC CTATGATTGGTTTGTGTCAAGAG
6035	Table 3A	Hs.5027	BE379724	9325089	601159415T1 cDNA, 3' end /clone=IMAGE:3511107 /clone_end=3'	-1	TGCTAGTTCAGGTCCTCCAGGCATTG ATTTGTACAGTTAACTCCGAGTG
6036	Table 3A	Hs.86437	BE464239	9510014	602411368F1 cDNA, 5' end /clone=IMAGE:4540096 /clone_end=5'	-1	ACAAGCATTTAGATCATACATGGTA AAGCCTATTACCAGCCAATGTTGT
6037	Table 3A	Hs.127428	BE466500	9512198	Homo sapiens, Similar to homeo box A9, clone MGC:18648 IMAGE:2987818, mRNA, complete cds /cds=(62,880)	-1	GGCCTACTGACCAAAATGTTGTGTTG AGATGATATTTAACTTTTGCCAA
6038	Table 3A	Hs.21812	BE467470	9513245	AL562895 cDNA /clone=CSODC021YO20-(3-prime)	-1	AAGTTTGTGCAGCACATTCCTGAGTG TACGATATTGACCTGTAGCCAGC
6039	Table 3A	Hs.122575	BE502246	9704654	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061)	-1	CGATAGAATTGAAGCAGTCCACGGG GAGGGGATGATACAAGGAGTAAACC
6040	Table 3A	Hs.279522	BE502919	9705327	hz81b08.x1 cDNA, 3' end /clone=IMAGE:3214359 /clone_end=3'	-1	ATAGACTCCAAAGAGGCGTTAAGCAC CTGGTTTTCTTTGGCTCAGAAAA
6041	Table 3A	Hs.197766	BE502992	9705400	clone 23932 mRNA sequence /cds=UNKNOWN	-1	CTCAAACGAAATTGGGCAGGCCATT GCGTGGTTTCTCTGGATAAGTTCC
6042	Table 3A	Hs.61426	BE550944	9792636	602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5'	-1	GCACATGACAGTAAGCGAGGTTTGG GTAATATAGATGAGGATGCCTAT
6043	Table 3A	Hs.201792	BE551203	9792895	7b55h12.x1 cDNA, 3' end /clone=IMAGE:3232199 /clone_end=3'	-1	TCCCAGAGTAAGTACAGTATCAAAT AGCAAGAGAGTTAGATGAGGACT
6044	Table 3A	Hs.122655	BE551867	9793559	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686)	-1	ACACAGGAACCGCTTACCCACCAGCT CTGCCCCGCTCTCTACCGCCATAG
6045	Table 3A	Hs.282091	BE552131	9793823	hw29b05.x1 cDNA, 3' end /clone=IMAGE:3184305 /clone_end=3'	-1	TTCTTCAAGAGAATAACCTATTAA GGCTAAAAATGGAAGCTCCAGT

Table 8

6046	Table 3A	Hs.146381	BE613237	9894834	RNA binding motif protein, X chromosome (RBMX), mRNA /cds=(11,1186)	-1	ACTGACCTAGCAGATGTGTGGAAAAG GAATCAGATCTTGATTCTTCTGGG
6047	Table 3A	Hs.4310	BE614297	9895894	eukaryotic translation Initiation factor 1A (EIF1A), mRNA /cds=(207,641)	-1	ACAACCTCAAGTGAAAAGATGTCTCCA GTTTCTGAAGATAACGCACGCTGA
6048	Table 3A	Hs.198802	BE621811	9892551	601493754T1 cDNA, 3' end /clone=IMAGE:3895836 /clone_end=3'	-1	CGCCGACTCGTTGAAAGTTTTGTTGT GTAGTTGGTTTTCGTTGAGTTCTT
6049	Table 3A	Hs.324481	BE646433	9970744	EST380617 cDNA	-1	CACCCACCTGGTAGGAAGGTCAATCT TATGCTCAGAAGTCCACCCACCA
6050	db mining	Hs.283165	BE646441	9970752	7e86h06.x1 cDNA, 3' end /clone=IMAGE:3292091 /clone_end=3'	-1	CAACTCCTTAAAGGGTTGAAGGTTGT GACAATACTGAGGGAAGTATGT
6051	Table 3A	Hs.341573	BE646470	9970781	tc38c11.x1 cDNA, 3' end /clone=IMAGE:2066900 /clone_end=3'	-1	AAAACACTCCACCTAAAAGCAGGAAA GATGGCAATTCTAAATAGCAGCTA
6052	db mining	Hs.283168	BE646492	9970803	7e87g01.x1 cDNA, 3' end /clone=IMAGE:3292176 /clone_end=3'	-1	GGAGGTTTTGATCGTGACTTTATTTT GAGATATTGTATCTTTGTTAGTATTGC
6053	Table 3A	Hs.187872	BE646499	9970810	7e87h02.x1 cDNA, 3' end /clone=IMAGE:3292179 /clone_end=3'	-1	TTGTAAGGTTCCGGGGAAGTCACTCA ACATGGTTCTCCAAGTCAAGGTTG
6054	db mining	Hs.283167	BE646510	9970821	7e88b08.x1 cDNA, 3' end /clone=IMAGE:3292215 /clone_end=3'	-1	TGTGAGTGTTATAGGTTACAGTGGAT TCCAAACTAGCCACAGTGAAGCA
6055	db mining	Hs.283168	BE646569	9970880	7e89c01.x1 cDNA, 3' end /clone=IMAGE:3292320 /clone_end=3'	-1	TCAGCCAGGAGGAAAAGCACTCTGAT TATGAATTGAGCAGAAGGAAACAA
6056	db mining	Hs.283169	BE646617	9970928	7e91b07.x1 cDNA, 3' end /clone=IMAGE:3292501 /clone_end=3'	-1	GTTCCCACTCGTTCTTGCCGGAGAAA CCTGCCCTTTCAAGCATATTCAA
6057	db mining	Hs.225200	BE646640	9970951	7e91f08.x1 cDNA, 3' end /clone=IMAGE:3292551 /clone_end=3'	-1	GGGTCCAAGATTATTGATTAATTTGG GCACCGCGAGAGCTCGAGTCCCCC
6058	Table 3A	Hs.129192	BE670584	10031125	7e36h08.x1 cDNA, 3' end /clone=IMAGE:3284607 /clone_end=3'	-1	GACCACCTGTAAAGCAAGTCCTTTCA AGTTTCACTGCACATCCCAAAACA
6059	Table 3A	Hs.75703	BE670804	10031345	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	TGGTCCACTGTCACTGTTTCTCTGCT GTTGCAAAATACATGGATAACACAT
6060	Table 3A	Hs.195374	BE671815	10032445	7a47c12.x1 cDNA, 3' end /clone=IMAGE:3221878 /clone_end=3'	-1	AGACTCTGGAAGGAGGGTCCGGAG TATTAACTGGCTGGGAATTGAGAGG
6061	Table 3A	NA	BE672733	10033274	7b75g07.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME OXIDASE	-1	TGAGAGCACACCATAAATTCACAGCA GGAATAACGAAGACACACGAGCA
6062	Table 3A	Hs.77542	BE673364	10033905	602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTTTGCTGAAGCTGAT TTGATTGGGTGCTGTTTCTCGC
6063	Table 3A	Hs.66357	BE673759	10034300	7d69d02.x1 cDNA, 3' end /clone=IMAGE:3278211 /clone_end=3'	-1	TGAGAAGGTAAAGTAGAAAGGGAAG ATGATGAGTGAACAATAAGCCTTGT
6064	db mining	Hs.283248	BE674662	10035284	7e93g03.x1 cDNA, 3' end /clone=IMAGE:3292756 /clone_end=3'	-1	ACATTATTCCATGGGAATAAGTCATC AGTGCAAAGGACTGTAAAGGAGTGC
6065	Table 3A	Hs.88845	BE674685	10035307	AV733781 cDNA, 5' end /clone=cdAASF08 /clone_end=5'	-1	CGCCGCTCCTGGAGACCTGATAACTT AGGCTTGAAATAATTGACTTGTCT
6066	Table 3A	Hs.171120	BE674709	10035331	7e94f05.x1 cDNA, 3' end /clone=IMAGE:3292833 /clone_end=3'	-1	TGTATGTGCAATATGCTTATGGGTAA TTATGGGCAAGAGAAATGAAACA
6067	db mining	Hs.283249	BE674713	10035335	7e94g02.x1 cDNA, 3' end /clone=IMAGE:3292850 /clone_end=3'	-1	ACCCCTTGGTAAAGCAGTTGTAAGAA TTAAACAAGAGGAATTGCTCTTTC
6068	Table 3A	Hs.167208	BE674762	10035230	7e98d05.x1 cDNA, 3' end /clone=IMAGE:3293193 /clone_end=3'	-1	AAATCAGGCCCTTGGCCATTACACA AAAATCCTTGTGAGATGACTCAAG
6069	db mining	Hs.283247	BE674807	10035275	7e93d11.x1 cDNA, 3' end /clone=IMAGE:3292725 /clone_end=3'	-1	AGGGCAGAGGTCCTTTGGGAGGGTA AGCTCACAAAACCTCAGGGAGGCAG
6070	Table 3A	Hs.174010	BE674902	10035443	7e97a04.x1 cDNA, 3' end /clone=IMAGE:3293070 /clone_end=3'	-1	TCATCTCCGCCAAGGTTCCCACTAGG CAGGAAAGGATTTTATCTAAAGT
6071	Table 3A	Hs.174144	BE674951	10035492	7e97g10.x1 cDNA, 3' end /clone=IMAGE:3293154 /clone_end=3'	-1	CCACCCAAGTCGGAATCCGAGTGAA ATAAATAGCATCGCCGCCAACTAC
6072	Table 3A	Hs.190065	BE674964	10035505	7f11b09.x1 cDNA, 3' end /clone=IMAGE:3294329 /clone_end=3'	-1	AGGCACAGGATTGTACCAATTCTCC CTTTACAAGCTGTATAATCAGTAA
6073	Table 3A	Hs.211828	BE675092	10035633	7f02d07.x1 cDNA, 3' end /clone=IMAGE:3293485 /clone_end=3'	-1	GCAACGCTGAATGTAGTAATGTGAC TCAGAGCTTCAAGTAAGCATTCG

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6074	db mining	Hs.330706	BE675125	10035666	IL3-UT0114-301100-357-H02 cDNA	-1	GCCACCCCATCTGGGAGGCCAGCA TCCAATTTCAGTCGCCTTCAATGATT
6075	db mining	Hs.283251	BE675180	10035721	7f03h06.x1 cDNA, 3' end /clone=IMAGE:3293627 /clone_end=3'	-1	TGATAGACTGGATGCTGCTATGGTAA TCTGCCTCAGGAAAATGCCGGACT
6076	db mining	Hs.339281	BE675338	10035879	HNC29-1-D4.R cDNA	-1	TGGAGCCAAGAAGCCACTGACTCAA GAGGATTTCAAGCGAGAGCTGCTTG
6077	db mining	Hs.283253	BE675379	10035920	7f08b02.x1 cDNA, 3' end /clone=IMAGE:3294027 /clone_end=3'	-1	CAACTTTTGTAAACAGGGGACTTAGCC GGGGGCAGGAGGGGTTCTTGAGAC
6078	db mining	Hs.283254	BE675403	10035944	7f08d10.x1 cDNA, 3' end /clone=IMAGE:3294067 /clone_end=3'	-1	ACTTGAAGGCACATCTTCTTTTGGT TGTTTTCCATCTTCAAATTAACCT
6079	db mining	Hs.283255	BE675434	10035975	7f09a10.x1 cDNA, 3' end /clone=IMAGE:3294138 /clone_end=3'	-1	TAAAACTGACATGACATGAGATGGT TTAAGTGTCAAACATAAGGGTCTTT
6080	db mining	Hs.283256	BE675531	10036072	7f10h08.x1 cDNA, 3' end /clone=IMAGE:3294303 /clone_end=3'	-1	ACTGACATAAGCCCACTTCAGGTGTT TGGAAGACACTAAAGAGAATCAGA
6081	db mining	Hs.315345	BE675610	10036151	7f12g09.x1 cDNA, 3' end /clone=IMAGE:3294496 /clone_end=3'	-1	GCAGCTTTTTGCTGGCGGGGCTCTA AATAAAGTAGCTTCCCAAAAGAAA
6082	db mining	Hs.180637	BE675718	10036259	7f14h04.x1 cDNA, 3' end /clone=IMAGE:3294679 /clone_end=3'	-1	ACCTGGTTATCTCGCAATGACCTAGC TAACACAAATGCAACATCAGCCGG
6083	db mining	Hs.283258	BE675792	10036333	7f16b02.x1 cDNA, 3' end /clone=IMAGE:3294795 /clone_end=3'	-1	TGATCAAAATGAAGATGCTCAACCG TATAAATGGCAGATGAAATAGACT
6084	db mining	Hs.283259	BE675819	10036360	7f17d10.x1 cDNA, 3' end /clone=IMAGE:3294931 /clone_end=3'	-1	GCAGGAGAGAAATACCTTCTAATGGG TGTGGACACTGGAGGAAGTGTAC
6085	db mining	Hs.283261	BE675957	10036498	7f19b06.x1 cDNA, 3' end /clone=IMAGE:3295091 /clone_end=3'	-1	AGGGCACTGTTTGTCTCTTAATATG GAGAAATATCGCAAATAACTGGGA
6086	db mining	NA	BE676019	10036560	7f20c12.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:3295222 3' similar to contains Alu repetitive element, m	-1	TTGGCCTATGTTAATTTCTATTCTCAG TTCTTCTGTGCCCTTCTCTCTCT
6087	Table 3A	Hs.170584	BE676049	10036590	7f21a03.x1 cDNA, 3' end /clone=IMAGE:3295276 /clone_end=3'	-1	GAACGTAAGCCCCGACGCTAGGCAGT GCTGTTAGAAAGTGATTTGAAGAG
6088	Table 3A	Hs.181015	BE676054	10036595	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA /cds=(165,2708)	-1	ATCCCATTTCTCCTCTCAAGGCAGGG GTCATAGATCCTAAGCCATAAAAT
6089	db mining	Hs.283263	BE676154	10036695	7f24a12.x1 cDNA, 3' end /clone=IMAGE:3295582 /clone_end=3'	-1	TGCTGTAAATGGCAGCTCCATAGGA ACCTATTTCCATAGGAACCTGCA
6090	db mining	Hs.283264	BE676173	10036714	7f24c12.x1 cDNA, 3' end /clone=IMAGE:3295606 /clone_end=3'	-1	ACTGGAGAAAGGTGTCTTCTGTCTCT TTCAGGGGCTCCTGCGGGGAATTC
6091	Table 3A	Hs.134648	BE676210	10036751	7f25c05.x1 cDNA, 3' end /clone=IMAGE:3295688 /clone_end=3'	-1	ATTATATTTGTCCCTATCAGAATCCTC GAATCCCTAGCAGCCAGTCCCTG
6092	db mining	Hs.283266	BE676275	10036816	7f26d04.x1 cDNA, 3' end /clone=IMAGE:3295783 /clone_end=3'	-1	TGCTCACTGTCTTCTGGAAGAGACAA GCACTTTCTTGAAATTCCTAAGCA
6093	Table 3A	Hs.158714	BE676408	10036949	7f29b11.x1 cDNA, 3' end /clone=IMAGE:3296061 /clone_end=3'	-1	CAATCGGATCATTCTTCTCAACTTGG GCGGCTCTTCTCCTCTCTCTCC
6094	Table 3A	Hs.220929	BE676472	10037003	cDNA FLJ14369 fis, clone HEMBA1001174, highly similar to ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 5 /cds=(207,746)	-1	TGCTTTGGGCAGTAGCTGAAGCCGA AGTATGAACAGTCCATTTGTITCT
6095	db mining	Hs.283268	BE676474	10037005	7f30c08.x1 cDNA, 3' end /clone=IMAGE:3296174 /clone_end=3'	-1	CACAGTTGAGTAGGAGGTCATGAAGA AGAAGAGATGATACCTGCCTTACC
6096	db mining	Hs.283269	BE676528	10037069	7f31d12.x1 cDNA, 3' end /clone=IMAGE:3296279 /clone_end=3'	-1	TTTGTGTAGCAATGTTTCATTAATTGC CTACTTTGTGCCAAATTCAGGCC
6097	Table 3A	Hs.123254	BE676541	10037082	AL572805 cDNA /clone=CS0D1034YH06-(3-prime)	-1	TCCAGCATGTATTGTCTATTGACAC ACAAAGTTTGAAAATAAAGGGGCA
6098	db mining	Hs.283505	BE676548	10037089	wh79f01.x1 cDNA, 3' end /clone=IMAGE:2386969 /clone_end=3'	-1	CACCCACCAGCCGAGGATTCACAAA GGGGGCGAAGGCGGAGAGCAAAGG
6099	db mining	Hs.283270	BE676613	10037154	7f33a08.x1 cDNA, 3' end /clone=IMAGE:3296438 /clone_end=3'	-1	TGGACTCTGTTTTCAAGAGGAAGAAA CAACTGACAAATAAGTTGATGCA
6100	db mining	Hs.283271	BE676614	10037155	7f33a10.x1 cDNA, 3' end /clone=IMAGE:3296442 /clone_end=3'	-1	ATGTTGAAACTGGTTTTAACTTGTAA GGTGTGGCTGATGTTACCCGACC
6101	db mining	Hs.283272	BE676667	10037208	7f34a07.x1 cDNA, 3' end /clone=IMAGE:3296532 /clone_end=3'	-1	ACACAGATTGAAGTCTACTGTTCTA AATGGCCTCTACTTCTGCTGCA

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6102	db mining	Hs.102165	BE676737	10037278	7f37g03.x1 cDNA, 3' end /clone=IMAGE:3296884 /clone_end=3'	-1	GGAACCTTCTGCTTCCACTTACGATGA AGGAACCTTGTAAGTCAATCCATCCA
6103	db mining	Hs.283276	BE676772	10037313	7f35d05.x1 cDNA, 3' end /clone=IMAGE:3296849 /clone_end=3'	-1	GAAGCCTTCTGTGGTCATAACAAGT CTCACACACCCCAAGGACTGATCT
6104	db mining	Hs.86761	BE738569	10152561	601572850F1 cDNA, 5' end /clone=IMAGE:3839581 /clone_end=5'	-1	GAGTCCAGCCTTTGAACCTGGCGCT GAATCCTGACTTTACTGCTTATTCA
6105	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAAATGTCTT TGCTCGAAATGGTATGCCAAAA
6106	Table 3A	Hs.293842	BE748663	10162655	601571679F1 cDNA, 5' end /clone=IMAGE:3838675 /clone_end=5'	-1	AAACTCATACATGCAGAAAAATGTCTT TGCTCGAAATGGTATGCCAAAA
6107	Table 3A	Hs.270293	BE857296	10371182	7g27b01.x1 cDNA, 3' end /clone=IMAGE:3307657 /clone_end=3'	-1	ACAAAAGTCATGGCTGTGAGGCTATC ATTACCCCTTTACCAAAGTTGGAA
6108	Table 3A	Hs.155935	BE858152	10373065	complement component 3a receptor 1 (C3AR1), mRNA /cds=(0,1448)	-1	AGTTCTATTTCATCCCAACTAAGCT ATGTGAAATAAGAGAAGCTACTTTGT
6109	Table 3A	Hs.294348	BE961923	11764299	601655335F1 cDNA, 3' end /clone=IMAGE:3845768 /clone_end=3'	-1	ATCCCGATGGTGCCACCGCTATTAA AGGTTCTGTTGTTCCACGATTTAA
6110	Table 3A	Hs.5181	BE962588	11765636	proliferation-associated 2G4, 38kD (PA2G4), mRNA /cds=(97,1281)	-1	ATGTCTCCATACCCATTACAATCTCC AGCATTCGCCCTCAACCTAAAAA
6111	Table 3A	Hs.314941	BE962883	11766238	602381893F1 cDNA, 5' end /clone=IMAGE:4499447 /clone_end=5'	-1	GCCCGTATTTACCCCTATAGCACCCCC TCTACCCCTTTAGAGCCCAAAAA
6112	Table 3A	Hs.301110	BE963194	11766612	601656811R1 cDNA, 3' end /clone=IMAGE:3865731 /clone_end=3'	-1	ACATTTTCTCCGCATAGCCTGCGT CAGATTAACACACTGAAGTACAA
6113	Table 3A	Hs.330887	BE963374	11766792	601657137R1 cDNA, 3' end /clone=IMAGE:3866193 /clone_end=3'	-1	CCAAGCTGGTTTCAAGCCAACCCCAT GGCCTCCATGACTTTTTCCAAAAAC
6114	Table 3A	Hs.334926	BE963551	11766970	Homo sapiens, clone MGC:8857 IMAGE:3866266, mRNA, complete cds /cds=(62,133)	-1	TGATCAGGTGAACCGGAAGTCTCCAA TTTCTGAATGGATTATGTTTCTAA
6115	Table 3A	Hs.316047	BE963666	11767085	601656685R1 cDNA, 3' end /clone=IMAGE:3865820 /clone_end=3'	-1	TGAGTACGTGACACTTGTGTAGAAT AGTGGTGTGAGCTATATCTTGT
6116	Table 3A	Hs.294578	BE963811	11767228	601657462R1 cDNA, 3' end /clone=IMAGE:3875846 /clone_end=3'	-1	GTGACCCTTGGCACCCGCTAGAAGTT TATGGCCGAGCTTTACCAATTAA
6117	Table 3A	Hs.302585	BE964028	11767356	601657601R1 cDNA, 3' end /clone=IMAGE:3875617 /clone_end=3'	-1	TGAACCTCAACTTTGACCAACCCATG AGACCCCTGTTATCCAACTTTCT
6118	db mining	Hs.210628	BE964051	11767519	601472729T1 cDNA, 3' end /clone=IMAGE:3875791 /clone_end=3'	-1	CCCTCTACTATTTGGCTCCATAACTTA GGACCTGCCTTTCCCGTTCCAG
6119	Table 3A	Hs.330588	BE964134	11767602	601151626F1 cDNA, 5' end /clone=IMAGE:3507774 /clone_end=5'	-1	CCCGTATTTACCCTATAGCACCCCT CTACCCCTTTAGAGCCCAAAAA
6120	Table 3A	Hs.252259	BE964149	11767617	ribosomal protein S3 (RPS3), mRNA /cds=(22,753)	-1	CCAACCTTCAGAACAGAAGGGTGGG AAACCAAGAACCGCTGCCATGCCCC
6121	Table 3A	Hs.184052	BE964596	11768078	PP1201 protein (PP1201), mRNA /cds=(75,1010)	-1	CGCCAGAAATCCAATCCAGCCCAA GGATATAGTTAGGATTAAATTACTTA
6122	Table 3A	Hs.286754	BE965319	11769559	601659229R1 cDNA, 3' end /clone=IMAGE:3895783 /clone_end=3'	-1	CTGAGATTTTGGGTTTTCCACACGGG CCAAGATACCCGGCCTCTGCTGAG
6123	Table 3A	Hs.297190	BE965554	11770044	601659486R1 cDNA, 3' end /clone=IMAGE:3896204 /clone_end=3'	-1	ATATCATTTCCACTTAGTATTATACCC ACACCCACCCAAGAACAGGGTTT
6124	Table 3A	Hs.108327	BF001438	10701713	damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAAACTGTTAGTACGCA TACCTCAGTTCAAACTTTAGGGA
6125	Table 3A	Hs.161075	BF001821	10702096	7g93g02.x1 cDNA, 3' end /clone=IMAGE:3314066 /clone_end=3'	-1	GCTTGCCCTAGCAGAGTCATACGGAA TAATGGAAACTCAACTTCTGTTT
6126	Table 3A	NA	BF056055	10809951	7k07h12.x1 NCL CGAP_GC8 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive eleme	-1	CACAATGCTGCCTCTCTGTGGATGA CTGATGGCAAGAGTCTGAATTGAA
6127	Table 3A	Hs.221695	BF058398	10812294	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	-1	CCTCTCACTCTCAGACTCCAAGGGCC AAGAAAACTACGGACAGGAAGCC
6128	db mining	Hs.255664	BF058429	10812325	7k30g11.x1 cDNA, 3' end /clone=IMAGE:3476949 /clone_end=3'	-1	GAGAGGAGGGGTCTCAGACGTTGGG GGACACTGCTGGGTGGGTGATTT
6129	Table 3A	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial cds /cds=(285,2942)	-1	TAAGAAATCCCAATTTTCAGGAGTGG TGGTGTCAATAAACGCTCTGTGGC
6130	Table 3A	Hs.144583	BF059133	10813029	Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	CGGCAGGGTGGCCTGTAACAATTTC GTTTTGCGAGAACATTCAGGTATT

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6131	db mining	Hs.257697	BF060727	10819637	AL533532 cDNA /clone=CS0DN004YJ14-(5-prime)	-1	GGGGCTCCCTTCCCGGCTTTGTTTTCTCTGGGAGATTTTATTTCCTAA
6132	Table 3A	Hs.193237	BF062295	10821193	7k76b11.x1 cDNA, 3' end /clone=IMAGE:3481293 /clone_end=3'	-1	GAAAGTGGAGGGAGTGACGGGGAGGAGACTAGCCAGAGAGGCTCATTAG
6133	Table 3A	Hs.174215	BF062628	10821538	7h62h05.x1 cDNA, 3' end /clone=IMAGE:3320601 /clone_end=3'	-1	CTTCTCCCTCTTGCCTCTGTGGTC TGATTTAAACGAAAGGTCGGAT
6134	db mining	Hs.159013	BF063675	10822585	hh82b10.x1 cDNA, 3' end /clone=IMAGE:2969275 /clone_end=3'	-1	GGACTTCTGAAATAGAGCTGGCTCCC TGGGGTGACAATGTATATATGCAA
6135	Table 3A	Hs.125887	BF109873	10939563	hypothetical protein FLJ14464 (FLJ14464), mRNA /cds=(69,3146)	-1	CTGGGTGTCGTGGAAGATGACGAAG ATGCTGGGCTGGCAGATGCAGCTCA
6136	Table 3A	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 /clone_end=3'	-1	ACCAGGGCTTAAACCTCAATTTATG TTCAATGACAGTGGGATTTTCTT
6137	Table 3A	Hs.250905	BF116224	10985700	hypothetical protein (LOC51234), mRNA /cds=(0,551)	-1	ATTCTCCAACCACAAACAGCACTTCT AAAACTAACTTTACTTTCTGCCCA
6138	Table 3A	Hs.318216	BF183507	11061818	601809991R1 cDNA, 3' end /clone=IMAGE:4040470 /clone_end=3'	-1	GATATAGTCTCCATACCCATTACCA TCTCCAGCCATCCCCCTCCAAC
6139	Table 3A	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTTGGTCTCTTTCCTGCTCA GGTCCCTTCATTTGTACTTTGGA
6140	Table 3A	Hs.232257	BF195579	11082611	RST2302 cDNA	-1	TAATACTGGAGGGGCTTGAAGAAGG CTGTCGTGTTTTGTCACTGCTTTG
6141	Table 3A	Hs.3353	BF197153	11085769	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGCTTTTCTTCCCTCACTA TGTAATTCAGTAGTCTCTCAGC
6142	Table 3A	NA	BF197762	11087169	7p91f02.x1 NCL CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA sequence	-1	AGGAAGAGCCTGCACCTGTGGTGGG ACAATCAGGGAAGGAAGTCAAAA
6143	Table 3A	Hs.50785	BF221780	11128957	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,766)	-1	TTTGGAGCTTCTATAGGAGTGGAGAG GGGCAGCTCATTTGTGAGAGTTGC
6144	Table 3A	Hs.250811	BF432643	11444806	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGAAAAACAATCCTGTA TCCCTCCCAAGAATCATGGGCT
6145	Table 3A	Hs.296356	BF433058	11445221	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TCATCCCTTAAACACTCTGTGATGGG ATCTTCAGGATCATCTTTGAAGT
6146	Table 3A	Hs.76611	BF433353	11445516	601435773F1 cDNA, 5' end /clone=IMAGE:3920562 /clone_end=5'	-1	TGCGTTTGGTTTAGGAATGTGCTTTT GTACTTCCACTTGAATAAAGGTGT
6147	Table 3A	Hs.178703	BF433657	11445846	AV716627 cDNA, 5' end /clone=DCBBCH05 /clone_end=5'	-1	TGCTCAGGACACATGCACAGACAT TTATCTCTGCACTCACATTTTGTG
6148	Table 3A	Hs.222833	BF435098	11447386	7p05g01.x1 cDNA, 3' end /clone=IMAGE:3645097 /clone_end=3'	-1	GGTTATTGCTGACACGCTGTCCCTCTG GCGACCTGTCGCTGGAGAGGTTGG
6149	Table 3A	Hs.293476	BF435621	11447923	hypothetical protein FKSG44 (FKSG44), mRNA /cds=(126,1520)	-1	CGTTTTCTGAGCATCCGTTGTGCCTT AACATTTTCTGCTTGTCTTTGGG
6150	db mining	Hs.257641	BF436704	11448943	7p07d12.x1 cDNA, 3' end /clone=IMAGE:3644999 /clone_end=3'	-1	CTTCTGAATCCCCGAGCTTCTCTTT TGTGCTCACAATGCCACCAATTC
6151	Table 3A	Hs.160980	BF437585	11449991	7p74d12.x1 cDNA, 3' end /clone=IMAGE:3651526 /clone_end=3'	-1	TGCTTACAAGGGTGATTGACCTTGCC TTACTCTTTATGTAATTTATGGCA
6152	db mining	Hs.258513	BF437915	11450432	AF150421 cDNA /clone=CBNCG12	-1	CTGGCGTATTACCATTTTGATAGCCT CTCTTCAGGCTAGATAAGCTGGGG
6153	Table 3A	Hs.126594	BF445163	11510224	nad21d12.x1 cDNA, 3' end /clone=IMAGE:3366191 /clone_end=3'	-1	CCCTGTATTATTGAAATGTCAGCATA ATGACTGGAAGGTGAAATTGGTCC
6154	Table 3A	Hs.174104	BF445405	11510543	601438710F1 cDNA, 5' end /clone=IMAGE:3923643 /clone_end=5'	-1	ACTGCTGTTGCATGAATAGATGATAC AAAGCAAGTGATGAGGTTGGTATG
6155	Table 3A	Hs.143389	BF446017	11511155	7p18a11.x1 cDNA, 3' end /clone=IMAGE:3646004 /clone_end=3'	-1	TGGAAGAACAAATTCAGACATCATCA GTAAGTCTTTAGGGACACAGGGAA
6156	Table 3A	Hs.295726	BF447885	11513023	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA /cds=(41,3187)	-1	AGTGAAGAACTGGTACAGTGTCTGCT TGATTTACAACATGTAACCTGTGA
6157	Table 3A	Hs.179526	BF475501	11546328	upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1), mRNA /cds=(221,1396)	-1	GCCAGAAAGTGTGGGCTGAAGATGG TTGGTTTCATGTTTTGTAATTATGT
6158	Table 3A	Hs.181311	BF478238	11549065	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGCTCTGAACTGAGTGAAGAAAT ATACTCTGCTTGTACCTGCGT
6159	Table 3A	Hs.179703	BF507849	11591147	tripartite motif protein 14 (TRIM14), mRNA /cds=(10,1230)	-1	CCATTTCACATCATGCCTTCCCTAC CTTCCTTCACAACCAATCAAGTG
6160	Table 3A	Hs.159673	BF508053	11591351	UI-H-B14-apx-b-11-0-ULs1 cDNA, 3' end /clone=IMAGE:3088845 /clone_end=3'	-1	ACACTTCCCTGAATGTTGAAGAAGAT ATGCTATCCATGCAATCCTTGTCG

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6161	Table 3A	Hs.158999	BF508694	11591992	UI-H-B14-aop-f-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3085601 /clone_end=3'	-1	ACTTGTGTTTGAACCACTTCTGCTTC CTCTTTAACCTGAGATGCACACGT
6162	Table 3A	Hs.77542	BF508702	11592000	602629438F1 cDNA, 5' end /clone=IMAGE:4754432 /clone_end=5'	-1	ACATTCTCTCATTTTGTCTGAAGCTGAT TTGATTGGGTGTCTGTTTCTCGC
6163	Table 3A	Hs.127311	BF508731	11592029	AU185774 cDNA /clone=B02302-013	-1	TGACAGAATGAAGTGGAAATGAAATC CCACAGTTATGATCGTAGTAGAGT
6164	Table 3A	Hs.144265	BF509758	11593056	UI-H-B14-agg-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3087390 /clone_end=3'	-1	AAGTACAGATGCCATCCCGGTGCTGT GATCTTCCAGCCATTCTCCATTTC
6165	Table 3A	Hs.256931	BF510393	11593691	zb02d05.s1 cDNA, 3' end /clone=IMAGE:300873 /clone_end=3'	-1	ACTGCCAATCTGATTAAAAATCTCCA AGCTTAATCTGTGCAACAAACA
6166	Table 3A	Hs.276341	BF510670	11593968	UI-H-B14-aof-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084615 /clone_end=3'	-1	GCCTGTTGTTCTGTTTATCGCCCTAT TTTACAAAACGTGATTCTGACCTGG
6167	Table 3A	Hs.248689	BF512500	11597602	UI-H-B13-ahw-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069162 /clone_end=3'	-1	AACCTGGCATTGCTAAGCCCCAGAAAA ATGTATTAGTGGACAGATGAAA
6168	Table 3A	Hs.136375	BF513274	11598453	602544150F1 cDNA, 5' end /clone=IMAGE:4666332 /clone_end=5'	-1	ACACTAGGTCCTTTTATACCTGTGCC TTTACGTTGTTTTCTGATTGCA
6169	Table 3A	Hs.300870	BF513602	11598781	mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	AATACAGATTCATTTATTTAAGCGTC CGTGGCACCAGACAGGAGCCCCAG
6170	Table 3A	Hs.255340	BF514247	11599426	UI-H-BW1-ani-h-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082601 /clone_end=3'	-1	AGTTCATCCCCCTTTCAGAAGCTGTTT GCTCTTGCTCATTAACCTGTGA
6171	Table 3A	Hs.283022	BF514341	11599520	triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCCTCTTTTCTGTATCACACAAGGG TCAGGGATGGTGAGTAAAGCTC
6172	Table 3A	Hs.83734	BF515538	11600717	syntaxin 4A (placental) (STX4A), mRNA /cds=(66,959)	-1	TGTTAGTGGCCCTCTGCATACCTATG GGAACTCAGTGATGTAATGCAAAAG
6173	Table 3A	Hs.146065	BF591040	11683364	AL580165 cDNA /clone=CS0DJ005YB18-(3-prime)	-1	CTGGGGCCGTAGCAAAATCATGAAA AACACTTCAACGTGTCTTTCAAT
6174	Table 3A	Hs.30841	BF592138	11684462	calcium channel, voltage-dependent, beta 2 subunit (CACNB2), mRNA /cds=(501,2318)	-1	TGCCAAGTCAGCAGATTGTGCTTTATG AATTACAGGGACTAGAAATGCCCA
6175	Table 3A	Hs.695	BF690338	11975746	cystatin B (stefin B) (CSTB), mRNA /cds=(96,392)	-1	TTGCATGTCTCTTCTAAATTTTCATTG TGTTGATTCTTAATCCTTCCCGT
6176	Table 3A	Hs.142838	BF732404	12057407	nucleolar protein interacting with the FHA domain of pK1-67 (NIFK), mRNA /cds=(54,935)	-1	AGAGTGAGAAGGCAGTTCAGCTTTTA GCACAGATTGTGTTATGTGTGAG
6177	Table 3A	Hs.296317	BF938959	12356279	mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCTACCTC TCCTTTTCTTCATCAGGTGTTCCCT
6178	Table 3A	Hs.182937	BF939014	12356334	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(44,541)	-1	TCCTGGGTGATACCATCAATGTCT TAATGTACTGTGGCTCAGACCTG
6179	Table 3A	Hs.26136	BF940103	12357423	hypothetical protein MGC14156 (MGC14156), mRNA /cds=(82,426)	-1	AATTCCAAAGGAGTGATGTTGGAATA TGCCCTCTAAGGGAGAGAAATGCA
6180	Table 3A	Hs.133372	BF940291	12357611	AF150127 cDNA /clone=CBCBGA01	-1	AGCCCTCCACCCCAACCCAGTCTTT TACAATGTGTTATTAAGACCCCT
6181	Table 3A	Hs.304900	BF980139	12347354	602288147F1 cDNA, 5' end /clone=IMAGE:4373963 /clone_end=5'	-1	CCATCCTTGAGAAATGTGGGCACCAA GTCCATATCTCAAATTAATCCAAT
6182	Table 3A	Hs.303214	BG054649	12511436	7a45b01.x1 cDNA, 3' end /clone=IMAGE:3576912 /clone_end=3'	-1	CGTTGCATTTTACATTTGTGTGGCA GGACAAGCATGGGGCAAGAGGGAC
6183	Table 3A	Hs.8258	BG054866	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1468)	-1	TATGAGTTTATGCGTTTTCCAGCCC TCCGAATCACTGACTGGGGCGTTT
6184	Table 3A	Hs.179661	BG056668	12521375	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	-1	TTGAAAAGATGACATCGCCCCAAGAG CCAAAAATAATGGGAATTGAAAA
6185	Table 3A	Hs.56205	BG057282	12522612	insulin induced gene 1 (INSIG1), mRNA /cds=(414,1247)	-1	TGCACTCTACCAGATTGAACATCTA GTGAGGTTACATTCATACTAAGT
6186	Table 3A	Hs.3709	BG057892	12523835	low molecular mass ubiquinone-binding protein (9.5kD) (QP-C), mRNA /cds=(77,358)	-1	TGGTGATATCTGCTTAGATTTCCTCG TATCTTTGCTGCCCTCCTTCAAGT
6187	Table 3A	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTGCAGCAGTTT CTCTACAGTTGTGCATAAATGTTT
6188	Table 3A	Hs.89104	BG058739	12525527	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAAGCATG AGTCAACCTGCTGGATAAACTTAGA
6189	Table 3A	Hs.166982	BG149747	12681777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTGGTTTGGTCAGCATACACACTTCT CATTTCAATTGATGTACACAGCCA
6190	Table 3A	Hs.100293	BG149986	12662016	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine: polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2039,4801)	-1	ACCTGGGATTTTCAATTTCTGCTGAAAG AAATAGGAAGAAGCAGGACTCACTT

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6191	Table 3A	Hs.198427	BG150273	12662303	hexokinase 2 (HK2), mRNA /cds=(1490,4243)	-1	GGGTGTGATGAATAGCGAATCATCTC AAATCCTTGAGCACTCAGTCTAGT
6192	Table 3A	Hs.313610	BG150461	12662491	7k01d08.x1 cDNA, 3' end /clone=IMAGE:3443006 /clone_end=3'	-1	AGCTTTACCACCTCGCAGTTGTAGA GATAGTCCCCGAAATATTATCCA
6193	Table 3A	Hs.184456	BG230563	12725596	hypothetical protein (LOC51249), mRNA /cds=(0,611)	-1	GTGTGAAGTGACAGCCTTGTGTGTGA TGTTTTCTGCCTTCCCCAAGTTTG
6194	Table 3A	Hs.89104	BG231557	12726684	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TGTTTTTAACAACCTCTCTCAACATTT TGTCAGGTTATTCTACTGTAACCA
6195	Table 3A	Hs.152925	BG231805	12726934	mRNA for KIAA1268 protein, partial cds /cds=(0,3071)	-1	TAAGTGGATTGGCAGACTCCTTGTGTG CTTAAGAGTGGCTTTCTAGGCAGG
6196	Table 3A	Hs.89104	BG231961	12727100	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	TGTTTTTAACAACCTCTCTCAACATTT TGTCAGGTTATTCTACTGTAACCA
6197	Table 3A	Hs.337986	BG235942	12749789	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGTCCTTCATTAAGCAAACTA
6198	Table 3A	Hs.3353	BG236015	12749862	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGTCTTTCTCTCAGCTA TGTAATTCAGTAGTCTCTCAGC
6199	Table 3A	Hs.75703	BG236084	12749931	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	GGTCCACTCTCACTCTTTCTCTGCTG TTGCAATACATGGATAACACCGT
6200	db mining	Hs.5146	D19756	500072	HUMGS00712 cDNA, 3' end /clone=mm0970 /clone_end=3'	-1	CATTCAGTATTTATTGGGAAGACTTG TCAAGCACCATGATAAGTGTGGGA
6201	db mining	Hs.237971	D19770	500086	hypothetical protein MGC5627 (MGC5627), mRNA /cds=(72,584)	-1	AGAGGGGGAAGGACTTACATGACAT CCTACTGGGAATTTGCTAGAAACCA
6202	db mining	Hs.30709	D20225	501322	HUMGS01199 cDNA, 3' end /clone=pm0880 /clone_end=3'	-1	CTGGTGAAGCTGACTCCCAAGTAAA GAGATATCAGCTCTGCTCAGACT
6203	db mining	Hs.30731	D20378	501474	HUMGS01352 cDNA, 3' end /clone=pm2943 /clone_end=3'	-1	TTGCTTCTCTGCTTTATAGAGTTCC CGTAAAAATACCCCTACCCCTGGC
6204	db mining	NA	D20425	501521	HUMGS01399 Human promyelocyte cDNA clone pm1281 3', mRNA sequence	-1	TCTGACCTCCGTGACGTTTATTACCA GCTGATGTCCGTACACTGATTCA
6205	db mining	Hs.228071	D20458	501554	HUMGS01432 cDNA, 3' end /clone=pm1542 /clone_end=3'	-1	GGGAAGGGTCAGCAACGATTTCTCA CCAAATCACTACACAGACAAAGG
6206	db mining	Hs.330221	D20465	501561	HUMGS01439 cDNA, 3' end /clone=pm2194 /clone_end=3'	-1	ACCCTAAATGGTTACACTACACCAA GACACTAAATGGCAGGGAGCCCT
6207	db mining	Hs.92440	D20522	501618	HUMGS01497 cDNA, 3' end /clone=pm1507 /clone_end=3'	-1	AAATTCAAATCACCCCTTGATCCAC TTCTTTCTCCCAACCAATCTGAT
6208	db mining	Hs.90165	D20538	501634	HUMGS01513 cDNA, 3' end /clone=pm1504 /clone_end=3'	-1	ACCATATCGTGCAAAATGTAATATGG AATTTCCAAACATCAATGAAGGGAT
6209	db mining	Hs.90171	D20572	501668	HUMGS01547 cDNA, 3' end /clone=pm1503 /clone_end=3'	-1	AATAAGTACCGTATATAAACACTTCTC TTTCTCTCCTCCCAATGGCAGC
6210	db mining	Hs.30766	D20726	504546	HUMGS01703 cDNA, 3' end /clone=mp0664 /clone_end=3'	-1	AGCATCACTCTTAGAAGAAGCAACTC CTTCCCTTGATTTCTGTATTGG
6211	db mining	Hs.5816	D20846	504666	HUMGS01827 cDNA, 3' end /clone=mp0825 /clone_end=3'	-1	TCAACCCAGAATCTATAATGTATGAA ATAAATTAATAGAGAACCCAACAGAT C
6212	db mining	Hs.30793	D20888	504708	HUMGS01869 cDNA, 3' end /clone=mp0836 /clone_end=3'	-1	AAGGTCTCCATCTAACAGGTAGAGCA GTTGGTGAGATGAGATGAGCCTG
6213	Table 3A	Hs.292590	D59502	960608	602626586F1 cDNA, 5' end /clone=IMAGE:4751396 /clone_end=5'	-1	GGTGATGATACCACTCCAAATGAACA GGGAAGCAAGTTCATCAGTCAACA
6214	Table 3A	Hs.119274	F13765	758015	RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4- binding protein) (GAP1IP4BP), mRNA /cds=(46,2550)	-1	AGCTGTTGGGGCTGCACTGAGCTGC AATTTTAAATGAGATTATAAATCT
6215	db mining	Hs.238797	H07915	872737	602081661F1 cDNA, 5' end /clone=IMAGE:4245999 /clone_end=5'	-1	AAGGAATTTGTTTTCCCTATCCTAACT CAGTAACAGAGGGTTTACTCCGA
6216	db mining	Hs.11307	H09541	874363	RST29274 cDNA	-1	CGCACACATTTTCTGTATGGACAAAT CCTGGATTGGCTTCGTTATTGGT
6217	Table 3A	Hs.187908	H69141	1030426	EST375312 cDNA	-1	GGTAATGAAACATCATCCAGTTAAC AATCAGCAAGGTTCTTCAGAGCCT
6218	Table 3A	Hs.117005	H71236	1043052	sialic acid binding Ig-like lectin 5 (SIGLEC5), mRNA /cds=(142,1797)	-1	TGGAAGAGTGGACTGAAGAAAGAACT TATACTCTCCCTCCTCTCAAAATGA
6219	Table 3A	NA	H78395	1056484	yu12f03.s1 Soares fetal liver spleen 1NFS cDNA clone IMAGE:233597 3' similar to contains Alu repet	-1	TCCTGGGCTATTGGCTTTATGATATC TTTTGAGAAACAGGATTTTCACTT
6220	Table 3A	Hs.38664	H80108	1058197	ILO-MT0152-061100-501-e04 cDNA	-1	ACCTTTTAAAGGATGTCTTATTTCCACC CCAACCTCTCCACTCCATTTTGTAGT
6221	Table 3A	NA	H92914	1099242	yt94g03.s1 Soares_pineal_gland_N3HPG cDNA clone IMAGE:231988 3', mRNA sequence	-1	GAACCTTCAAACTGTCACTTTGAGT TCCAGAAGAGTCTTCAGCATCTT
6222	Table 3A	Hs.2210	L40410	703109	thyroid receptor interactor (TRIP3) mRNA, 3' end of cds /cds=(0,458)	-1	GTATTTGGGCTTCTCCAAGCAGTCA CGCAGACGAGGCTGTACATTTGA
6223	Table 3A	Hs.2200	L40557	705359	perforin 1 (preforming protein) (PRF1), mRNA /cds=(0,1667)	-1	CAAGCATACTGGTCTTTTCAAGCTC ACTGTTCTCACCACACGGCCCCAC

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6224	Table 3A	Hs.198726	M24069	181483	vasoactive intestinal peptide receptor 1 (VIPR1), mRNA /cds=(56,1543)	-1	TCCATATCCATTTCTGACGTTGAACC ATTTGACAGTGCCAAGGACTTTGG
6225	Table 3A	Hs.132911	N20190	1125145	MR2-OT0079-290500-007-b03 cDNA	-1	AAGCCTGTTTTTCACTCTAAAAATTC AGAGGACACGCTAAGAACGATCA
6226	Table 3A	Hs.323950	N23307	1137457	zinc finger protein 6 (CMPX1) (ZNF6), mRNA /cds=(1265,3381)	-1	CCTCAGCTTCCAACCTCTGATTCCAGG ACAGGATGGAAAACCTTTGGACAG
6227	Table 3A	Hs.32250	N30152	1148672	yx81f03.s1 cDNA, 3' end /clone=IMAGE:268157 /clone_end=3'	-1	GCGCACATGGCTATTTTGATACACAA AGTTGTGTTTGTCTACTTTAGAAGC
6228	db mining	Hs.44512	N33584	1153983	yv21f11.s1 cDNA, 3' end /clone=IMAGE:243405 /clone_end=3'	-1	AACTCACGACAATTGCTACAAAACAC CAGGGAGGGGCTTTTGTGTTTTT
6229	Table 3A	Hs.3353	N36787	1157929	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTTCCCGTCTTTCTCCTCACCTA TGTAATTTCACTAGTCTCTCAGC
6230	Table 3A	Hs.38218	N39230	1162437	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	GCCCTGGTATGTATGCCTTTCTCTCC TACTGTCTAATAGCACCTCGTAAA
6231	Table 3A	Hs.236456	N49836	1191002	602287746T1 cDNA, 3' end /clone=IMAGE:4375057 /clone_end=3'	-1	AAGAAACCGTGGAAGATACTGGTTTA TTTCAAATGAGCAGAGTATGTTGT
6232	Table 3A	Hs.114453	N58052	1201942	601880526F1 cDNA, 5' end /clone=IMAGE:4109119 /clone_end=5'	-1	CCACCTCTTCTGACATGAATGTAGCA TAAGTTAGCAATCGGTTCTTCCAA
6233	Table 3A	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	AGGTTCCCTTTCAAATAAAGATAAAG AATTTGACTTGGGACACTGCCAGA
6234	Table 3A	Hs.205555	N72600	1229704	za46f08.r1 cDNA, 5' end /clone=IMAGE:295623 /clone_end=5'	-1	GGCTGGCCTCATTTTGAAAAGTTAGT ACAATTTTCTTCAGTGCTCACTTG
6235	Table 3A	Hs.256931	N80578	1243279	zb02d05.s1 cDNA, 3' end /clone=IMAGE:300873 /clone_end=3'	-1	ACTCCAGAACGTCAGAAATGGTGTAG CAGAAATGAATCTGTTATAGGAA
6236	Table 3A	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942 /clone_end=3'	-1	CTGTTCGAAAGTTGGAGACTGCCTGT ACCCAGGTTGATAGTCAATTTGTTT
6237	db mining	Hs.118964	NM_017660	8923093	hypothetical protein FLJ20085 (FLJ20085), mRNA /cds=(62,655)	-1	CCACCTTGAGCGCCTTCTCTGGTTG GTTGTCTGCACTGCTCTCACACATG
6238	Table 3A	Hs.11594	R12665	765741	yf40a04.s1 cDNA, 3' end /clone=IMAGE:129294 /clone_end=3'	-1	ACCCCTTCCCTTTTTCATATCCTTTCT TCAAAAATCTAAATGATGTGCCT
6239	db mining	Hs.108082	R40823	821181	602068988F1 cDNA, 5' end /clone=IMAGE:4067972 /clone_end=5'	-1	AGTTCAGGAGGTGGTTTAAATATT GGATGAAAACCTACAGGCTGTTTT
6240	db mining	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTTACAAGCCATCTTTAC ATGCATTAAACGAGGGCTACAAC
6241	Table 3A	Hs.94881	R50838	812740	602387586F1 cDNA, 5' end /clone=IMAGE:4516388 /clone_end=5'	-1	ACAATACATTTACAAGCCATCTTTAC ATGCATTAAACGAGGGCTACAAC
6242	RG housekeeping genes	Hs.92004	R52541	814443	HSU55967 cDNA /clone=39883	-1	GGCCTGAAGAAGGAGATAAGTGTTT CATTGGGCAACATAAGAGAAGTTAA
6243	RG housekeeping genes	Hs.26766	R60313	831008	602270716F1 cDNA, 5' end /clone=IMAGE:4359027 /clone_end=5'	-1	TCCATCCCAAAGGAGAGCTACTGTAC TGACTGTACTTGTGGAATGCAGCG
6244	db mining	Hs.330530	T25714	563034	ESTDIR309 cDNA, 3' end /clone=CDDIRX9 /clone_end=3'	-1	ACCCACCACTCTCAGGACCACCTGAA GGCAGAATAAACCGGATCCTGTTG
6245	db mining	NA	T25727	563047	ESTDIRX51 CD34+DIRECTIONAL cDNA clone CDDIRX51 3', mRNA sequence	-1	AAATTGTGTGAGAAGGCTGATAAAGC TCTGTGGTTTCTCCCTGTGCTATT
6246	db mining	Hs.7569	T26893	567784	ESTDIR465 cDNA, 3' end /clone=CDDIR465 /clone_end=3'	-1	GCTGGGCTTCTGCAAAATTATAAAGT TGCTTTATTAAATTCATACATGCGG
6247	db mining	Hs.172822	T26903	567794	ESTDIR551 cDNA, 3' end /clone=CDDIR551 /clone_end=3'	-1	AGCTGATTCATTCTATGTGTGC CACTAAATAAAGAGATTGAGCAAGT
6248	Table 3A	Hs.185675	T98171	747516	QV2-EN0098-010201-603-a05 cDNA	-1	CCTGAAAGCTGTGTTGGTCCCTGTGA CCTTCCAATGCAATCTAGACTGTG
6249	Table 3A	Hs.58066	W72392	1382348	602389077F1 cDNA, 5' end /clone=IMAGE:4517875 /clone_end=5'	-1	CTCATACACTTCTCAGCCTCAGCACC TAACCCCTCACACAACACTCCAGTA
6250	Table 3A	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTTGTGGGGCGGGTAT GTCTGTATATAATCTGTGCAGCCA
6251	Table 1	NA	AA136584	1697794	zn95b02.s1 Stratagene fetal retina 937202 cDNA clone IMAGE:565899 3', mRNA sequence	-1	AACATATCCAGGAGGACAAAACCTCTG GGCTGGACAATGTATCCACAAGGG
6252	Table 1	NA	AA431959	2115667	zw77a03.s1 Soares_testis_NHT cDNA clone IMAGE:782188 3', mRNA sequence	-1	AGAGCAAGTCTCAGAAAATGCTGT ATCTACACTGTCTATGTTTGCCA
6253	Table 1	NA	AA482019	2209697	zu98e04.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:746046 3', mRNA sequence	-1	ACCACCAGCTATTTGTAATTCCTTCTT CTAAGGCATAGTAAAACCTTGCT
6254	Table 1	NA	AA524720	2265648	ng42e03.s1 NCI_CGAP_Co3 cDNA clone IMAGE:937468 3', mRNA sequence	-1	GGACGGTTGGCTGAATGGCAACAGT GATGGAATATTATATTTAGCCACA

Table 8

6255	Table 1	Hs.57787	AA588755	2402486	602381381F1 cDNA, 5' end /clone=IMAGE:4498845 /clone_end=5'	-1	AGGTTGTTATCAGGTGGCACAAATTA AATCCATCTTGAAGACTTCACACA
6256	Table 1	NA	AA628833	2541220	af37g04.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1033878 3', mRNA sequence	-1	GACTCGTTACGCCGTAGTTTGTCTTA TCTTGTATCAAAATGAATTCGT
6257	Table 2	Hs.180669	AA633203	2556617	OS-4 protein (OS-4) mRNA, complete cds /cds={305,1156}	-1	AGAGCTATGGGTGCTACAGGCTTGTC TTTCTAAGTGACATATCTTATCT
6258	Table 1	Hs.239489	AA639796	2563575	TIA1 cytotoxic granule-associated RNA- binding protein (TIA1), transcript variant 2, mRNA /cds={185,1345}	-1	ACCCTTATAAACAGAGCCAGGAAA GACAGCTCGAGTGATAATCTCT
6259	Table 1	Hs.29282	AA748714	2788672	mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA /cds={83,1963}	-1	AGCTCCTCCCTCTCAACACCCAGTTT CCTGGGAGTTGTCATTAAGGAA
6260	Table 1	Hs.111554	AA806222	2874972	ADP-ribosylation factor-like 7 (ARL7), mRNA /cds={14,592}	-1	GCTGTAATTCCTGCTCATCATCCTT CTCTTTTGTTCATGACCTTTT
6261	Table 1	NA	AA806766	2875518	ob91d04.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1338727 3', mRNA sequence	-1	TCGCTTTTCAACTGATTCCATTCAC CATGTCAATACTCCTGGGCTGCT
6262	Table 1	Hs.226755	AA909983	3049273	RC1-UT0033-250800-022-h02 cDNA	-1	ATCCAAGCTTTAATCTGCCATCTCA GAATGGTGATAAACCATTTCTCCC
6263	Table 1	Hs.50252	AA984245	3162770	mitochondrial ribosomal protein L32 (MRPL32), mRNA /cds={46,612}	-1	TCAGCCAACTGAATCTGGTATCTTT ACTTAAACAGCAGGTTGTAGTTA
6264	Table 1	Hs.53542	AI084224	3422647	chorea-acanthocytosis (CHAC) mRNA, complete cds /cds={260,9784}	-1	TCATAGTTGTGAAATCTTCTCAGG CTCCTTAAACCTCGCTTTGTTGT
6265	Table 1	Hs.135167	AI091533	3430592	AV712376 cDNA, 5' end /clone=DCAAND12 /clone_end=5'	-1	AGAGGCAACACTTAAACACTAGGGCT ACTGTGGCATCTGTAGACAGCA
6266	Table 1	Hs.11637	AI275205	3897479	602388093F1 cDNA, 5' end /clone=IMAGE:4517086 /clone_end=5'	-1	TGACTTTCAGGAATGTCAGCATTGAC CTCTCCTTGCCACTGTTACTCAGC
6267	Table 1	Hs.8724	AI298509	3958245	serine threonine protein kinase (NDR), mRNA /cds={595,1992}	-1	TCTCAAGAGAGAACGCCACAGCAGA GAGACCCAATCCGCCTAAGTTGCAG
6268	Table 1	Hs.142838	AI299573	3959158	nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA /cds={54,935}	-1	AGAGTGAGAAGGCAGTTCAGTTTTA GCACAGATTTGTTTATGTGTTTCA
6269	Table 1	Hs.100555	AI352690	4089896	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds={71,2083}	-1	GGGGTAGGAAGAGGATGGAATTGAG ATGTTTGAGCCTCATTTACATCAAT
6270	Table 1	Hs.108124	AI362793	4114414	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	GCTCGCTACCAGAAATCCTACCGATA AGCCCATCGTGACTCAAACTCAC
6271	Table 1	Hs.134342	AI363001	4114622	mRNA for LanC-like protein 2 (lanc2 gene) /cds={186,1538}	-1	GACGCGCACACCTTGAGTGACAG CGACTCTTCTCTACAGGTTTCC
6272	Table 1	Hs.192427	AI380016	4189869	602298277F1 cDNA, 5' end /clone=IMAGE:4390770 /clone_end=5'	-1	ACTTCCCTTTAGGTATCCCTGGAGT AATAATGACAACAAATTCACCTGC
6273	Table 2	Hs.158976	AI380390	4190243	UI-H-BI2-ah1-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2726692 /clone_end=3'	-1	GTCCTTTGATAGCAGAACAGAGGCT CTGTGATCCTCTGGACCTCAGATT
6274	Table 1	NA	AI392705	4222252	tg23b03.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2109581 3', mRNA sequence	-1	TGCAGGCTCATTGTGCTCCTTCTTCT GGGTTTCAATTGGATTTCAGTCC
6275	Table 1	Hs.76239	AI393970	4223517	hypothetical protein FLJ20608 (FLJ20608), mRNA /cds={81,680}	-1	GAGGACTGGGACCGTGATTCCACTA ACCGGAAACCGTCGCCTTTCGGGCC
6276	Table 1	Hs.79968	AI419082	4265013	splicing factor 30, survival of motor neuron-related (SPF30), mRNA /cds={0,716}	-1	GGATGTGTGATGTTTATATGGGAGAA CAAAAAGCTGATGTATAGCCCTGT
6277	Table 1	Hs.121973	AI458739	4311318	602428025F1 cDNA, 5' end /clone=IMAGE:4547239 /clone_end=5'	-1	CCTGCAACAGCTAAGGCCAAGCCAA ACTTACCGTGGACTCAAACACTTTG
6278	Table 1	Hs.342008	AI498316	4390298	UI-H-BI1-aeq-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2720188 /clone_end=3'	-1	GCCAGAATGGTACAGAGTGGAGGGT GTTCTGCTAATGACTTCAGAGAAGT
6279	Table 1	Hs.194054	AI523854	4437989	HA0689 cDNA	-1	GACAAAATAGTTACCTATGCTTTCCTT CTGGCACCCCGAATGTACGCAGG
6280	Table 1	Hs.14623	AI571519	4534893	Interferon, gamma-inducible protein 30 (IFI30), mRNA /cds={40,951}	-1	AAGCCAGATACACAAAATCCACCC CATGATCAAGAATCCTGCTCCACT
6281	Table 1	Hs.278554	AI627495	4664295	chromobox homolog 3 (Drosophila HP1 gamma) (CBX3), mRNA /cds={111,662}	-1	TGCTGAAAGTGGTCCCAAAGGGGTA CTAGTTTTTAAAGCTCCCAACTCCCC
6282	Table 1	Hs.17132	AI633798	4685128	602326676F1 cDNA, 5' end /clone=IMAGE:4427970 /clone_end=5'	-1	GCAACTGTTTTCTAGGACATGTTTAC TAGAACTACTTTAAGTATGCTGTGC
6283	Table 1	Hs.4283	AI651212	4735191	602621616F1 cDNA, 5' end /clone=IMAGE:4755315 /clone_end=5'	-1	ACAGTTACTTTGGAGCTGCTAGACTG GTTTTCTGTGTGGTAAATTGCCCT
6284	Table 1	Hs.324507	AI678099	4888281	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds={182,2056}	-1	CGCCAGAGGTGAGAACATGTCTATTT TGAATTGGATCGTTACAAATGAGC
6285	Table 1	Hs.90744	AI684022	4895316	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA /cds={0,1268}	-1	TTCTGACACGATTACACACGAGGCT TTAATGCCATTTGGGTAGGTGAGC

Table 8

6286	Table 1	NA	Al688560	4899854	wd39f08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2330535 3', mRNA sequence	-1	ACTGAAAAGTTGAAAGACTTTTGCAG TGAACATTTATATACTCCCGCT
6287	Table 1	Hs.177708	Al697756	4985656	602369210F1 cDNA, 5' end /clone=IMAGE:4477370 /clone_end=5'	-1	TGGTTCCTGTGCTCACCATAGGGCTG GTGTACATTGGGCCATTAATAAAC
6288	Table 1	Hs.80887	Al701165	4989065	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN), mRNA /cds=(297,1835)	-1	TCTGGGAAAGACATTTTAAAGCTGCT GACITTCACCTGCAAAATCTAACAG
6289	Table 1	Hs.299883	Al742850	5111138	hypothetical protein FLJ23399 (FLJ23399), mRNA /cds=(282,1769)	-1	TGTTTTACCTCACTGTTGGACATACAT TCCAAGCTTTTCAACTCTAGGAG
6290	Table 1	Hs.14373	Al760353	5176020	yx2b11.1.r1 cDNA, 5' end /clone=IMAGE:262917 /clone_end=5'	-1	TTTATCTCAGAATCTTGATGAACCTCTG AAATGACCCCTGATGGGGGCATG
6291	Table 1	Hs.36137	Al765153	5231662	hepatocyte nuclear factor 3, gamma (HNF3G), mRNA /cds=(0,1043)	-1	CCGGGAAGCGGGTACTGGCTGTGT TTAATCATTAAAGGTACCGTGCCG
6292	Table 1	Hs.195175	Al802547	5368019	mRNA for CASH alpha protein /cds=(481,1923)	-1	AGCCCTTTCTTGTTGCTGTATGTTA GATGCTTTCCAATCTTTTGTTACT
6293	Table 1	Hs.25648	Al803065	5368537	tumor necrosis factor receptor superfamily, member 5 (TNFRSF5), mRNA /cds=(47,880)	-1	GGGGTATGGTTAGTAATATCCACCA GACCTTCCGATCCAGCAGTTTGGT
6294	Table 1	NA	Al807278	5393844	wf38h03.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2357909 3', mRNA sequence	-1	CTCTACCATAAGGCACATATCAGAGAC TGCTACTGGAGTGATATTGGTT
6295	Table 1	Hs.220850	Al880607	5554656	ym91d11.1 cDNA, 5' end /clone=IMAGE:166293 /clone_end=5'	-1	TGGGGCATTGAAAACCTTCACAGGC CCACTGCTGCTGCTGAAATAAAA
6296	Table 1	Hs.23096	Al884671	5589835	602254146F1 cDNA, 5' end /clone=IMAGE:4346626 /clone_end=5'	-1	TGGCGAGGATAAATAGAGGCATGTT TTTGCTACTTTCATATCATTTGGC
6297	Table 1	Hs.179391	Al917642	5637497	wi52d11.x1 cDNA, 3' end /clone=IMAGE:2393877 /clone_end=3'	-1	GCAGGAAAGATGGGGTGGTGGACTG TTTTGCCTACTTTTTGTTTTGAA
6298	Table 1	Hs.180446	Al948513	5740823	importin beta subunit mRNA, complete cds /cds=(337,2967)	-1	CAGGGTATCAGATATTGTGCTTTTTG GTGCCAGGTTCAAAGTCAAGTGCC
6299	Table 1	Hs.7557	AL042081	5421426	FK506-binding protein 5 (FKBP5), mRNA /cds=(153,1526)	-1	AGGCTGCATATGGATTGCCAAGTCAG CATATGAGGAATTAAGACATTGT
6300	Table 1	Hs.39911	AL138429	6855110	mRNA for FLJ00089 protein, partial cds /cds=(62,1111)	-1	TTAAGAACCCCAAAGATTAAAGGAAA CAATGTTAAGGGCTTTTGTGAGGA
6301	Table 1	Hs.13144	AL521097	12784590	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	-1	GATACACTGTCCAGCCAGGTCCAG GCCCTAGGTTCTTACTCTAGCTAC
6302	Table 1	Hs.26670	AL540260	12870241	AL540260 cDNA /clone=CS0DF032YF03-(3-prime)	-1	ACTCAGGTGGTGTGTTAGTGAT GCTGGAGAAGAGAAATATTACTGT
6303	Table 1	Hs.183232	AL561892	12909772	hypothetical protein FLJ22638 (FLJ22638), mRNA /cds=(12,476)	-1	AAACACAGCCACCCCATTTTCAGACC GCCTTCCTGAGGAGAAATGACAG
6304	Table 1	Hs.5057	AL578975	12943566	AL578975 cDNA /clone=CS0DK012YN01-(3-prime)	-1	TTGGCCCAAGTGTGATTGCTTTTA TCTTTGGTACTTTTACTTGAATGG
6305	Table 1	Hs.198298	AL582354	12950255	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), mRNA /cds=(297,5015)	-1	AGCCTGAGGCAAAATAAAATCCAGTA ATTTCGAAGAATGGGTGTTGGCAA
6306	Table 1	Hs.101370	AL583391	12952309	AL583391 cDNA /clone=CS0DL012YA12-(3-prime)	-1	AGGACCTTGACAAGCCGTTTGAGATG GAATGTAGGCCCTGATGTTATGCT
6307	Table 1	Hs.38218	AV659358	9880372	602569369F1 cDNA, 5' end /clone=IMAGE:4693744 /clone_end=5'	-1	TGTAAGTTGACTTTCAAAAGTCTCTG GAAACACTGGACTTTAGCTGGTCC
6308	Table 1	Hs.301704	AW002985	5849991	eomesodermin (Xenopus laevis) homolog (EOMES), mRNA /cds=(0,2060)	-1	AACAAGCCATGTTGCCCTAGTCCAG GATTGCCTCATTGAGACTTGCTA
6309	Table 1	NA	AW027160	5885916	wf72b08.x1 Soares_thymus_NHFTh cDNA clone IMAGE:2512983 3' similar to contains Alu repetitive element	-1	ACCGCCAAAGCCAATCATCCACTTTC AGTACTTACCTAACCAATCTCCCA
6310	Table 1	Hs.89433	AW071894	6026892	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (ABCC1), transcript variant 1, mRNA /cds=(196,4791)	-1	TTTGGGGGATCCTTTTGAATGACTT ACACTGGAATGCGAACATTTGCA
6311	Table 1	Hs.335449	AW136717	6140850	UI-H-B1-adm-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2717092 /clone_end=3'	-1	TTCTGGCCTGTTCACCTAGAAACGC TATTTCTGTGTATGTTCTGGC
6312	Table 1	Hs.12035	AW137149	6141282	602122419F1 cDNA, 5' end /clone=IMAGE:4279300 /clone_end=5'	-1	GGGTTACATTTGAGTCTCTGTACCTG CTTGGAAGAAATAAAATACGTGT
6313	Table 1	Hs.337727	AW161820	6300853	au70h03.x1 cDNA, 3' end /clone=IMAGE:2781653 /clone_end=3'	-1	TGTGGGCTGGGTATAAACCTACTTT GTGATTTGCTAAAGCAGAGATGT
6314	Table 1	Hs.81248	AW166442	6397967	CUG triplet repeat, RNA-binding protein 1 (CUGBP1), mRNA /cds=(137,1585)	-1	ACTGGCAATGAAGCATACTGGCTTG CAGGGACCTTCTGATTCAGTACA
6315	Table 1	Hs.166975	AW293159	6699795	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(218,541)	-1	CTCCCATCATTCCTCCGAAAGCCA TTTTGTTCAAGTGGCTCATCCAGC
6316	Table 1	Hs.328348	AW338115	6834741	tp39g05.x1 cDNA, 3' end /clone=IMAGE:2190200 /clone_end=3'	-1	GGCGTTTCCCATGACCAAGTTTGACC CTGGTTTGAATAAGAGAAGTGCC

Table 8

6317	Table 1	Hs.337988	AW440517	6975823	Homo sapiens, clone MGC:17431 IMAGE:2984883, mRNA, complete cds /cds=(1336,1494)	-1	GCCAGTCTCTATGTGTCTTAATCCCT TGTCCTTCATTAAGCAAACTA
6318	Table 1	Hs.250	AW444632	6986394	xanthene dehydrogenase (XDH), mRNA /cds=(81,4082)	-1	TGCAATGAGGCAGTGGGGTAAGGTT AAATCCTCTAACCGCTCTTTGAATCA
6319	Table 2	Hs.335815	AW444812	6986574	UI-H-B13-ajy-d-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733380 /clone_end=3'	-1	TGGCAACTTCAACTCCTTGATGGCGA TAATCTCTGGTATGAATATGAGCC
6320	Table 1	Hs.342873	AW451293	6992069	RC3-HT0230-130100-014-g06 cDNA	-1	TGCTTGGGAAATTTGGTTTGTAACC TAAATAGCCCTTATTTCTGGGGA
6321	Table 1	Hs.342735	AW452096	6992953	UI-H-B13-alo-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3068186 /clone_end=3'	-1	CTTCTGCGCTGAAGCTGCCCCCATGA CTCCCTCTTTGTGCAAAAGCATG
6322	Table 1	Hs.80618	AW510795	7148873	hypothetical protein (FLJ20015), mRNA /cds=(31,522)	-1	ACCCAGTTTGTGCATAGTTCATGATC CTCTATAAAACCAGCTTTTGTGGA
6323	Table 1	Hs.259842	AW614193	7319379	cDNA FLJ11025 fis, clone PLACE1003968, moderately similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT /cds=(159,1145)	-1	ACACCATTTTCAGCGTTGGATCACAGA CAGCTCTTCTTTATATCCAGCA
6324	Table 1	Hs.334437	AW778778	7793371	hypothetical protein MGC4248 (MGC4248), mRNA /cds=(70,720)	-1	TGGCATAATGTTGGATTGAATCTACA TTTTGGCAGAGTTAAACATTTCCC
6325	Table 1	Hs.151393	AW778854	7793457	glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA /cds=(92,2005)	-1	AGAATGGCTGGTTTTCGTTTGCAATT TGCTTGTGTAATCAGGTTGTAAA
6326	Table 1	Hs.120243	BE044364	8361417	gamma-parvin (PARVG), mRNA /cds=(0,995)	-1	ATCGTTGGATTATCTTTGAACCCCTT TGTGTGGATCATTTTGAGCCGCTT
6327	Table 1	Hs.5734	BE218938	8906256	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(395,3145)	-1	ATACAGGGTTCATCCAGAAAGCATT CAGTCAGAGCAAGTTAAAGTCAGT
6328	Table 1	Hs.167988	BE222301	8909619	neural cell adhesion molecule 1 (NCAM1), mRNA /cds=(201,2747)	-1	AAGTTGCTCTGTGCTAAAGCAAGCGT GGGATGATCCTACCTACCTCAGG
6329	Table 1	Hs.27774	BE348809	9260662	602386841F1 cDNA, 5' end /clone=IMAGE:4515730 /clone_end=5'	-1	AGCTAGTGATGTTTGTCCAAAGGAA GATTCTGACAAAGCTTCAGCAGA
6330	Table 1	NA	BE348955	9260808	hs91h01.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:3144625 3', mRNA sequence	-1	ACACAGACATATTGACCGCACACAAC ACTGAAATGGACTGACTTGAGAAA
6331	Table 1	Hs.56156	BE349148	9261087	601463367F1 cDNA, 5' end /clone=IMAGE:3866512 /clone_end=5'	-1	TGGTTCTCTGATTGTGAATGAGCACC TGGATATGTCAATTAATGCCCA
6332	Table 1	Hs.127428	BE466500	9512198	Homo sapiens, Similar to homeo box A9, clone MGC:19648 IMAGE:2987818, mRNA, complete cds /cds=(62,880)	-1	GGCCTACTGACCAAAATGTTGTGTTG AGATGATATTTAACTTTTGCCAA
6333	Table 1	Hs.122575	BE502246	9704654	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4), mRNA /cds=(6,1061)	-1	CGATAGAATTGAAGCAGTCCACGGG GAGGGGATGATACAAGGAGTAAACC
6334	Table 1	Hs.197766	BE502992	9705400	clone 23932 mRNA sequence /cds=UNKNOWN	-1	CTCAAACGAAATTGGGCAGGCCATTT GCGTGGTTTCTCTGGATAAGTTCC
6335	Table 1	Hs.61426	BE550944	9792636	602329933F1 cDNA, 5' end /clone=IMAGE:4431248 /clone_end=5'	-1	GCACATGACAGTAAGCGAGGTTTTGG GTAATATAGATGAGGATGCCTAT
6336	Table 1	Hs.122655	BE551867	9793559	hypothetical protein MGC14425 (MGC14425), mRNA /cds=(318,686)	-1	ACACAGGAACCGCTTACCCACCAGCT CTGCCGCGTCTCTACCGCATAG
6337	Table 1	Hs.4310	BE614297	9895894	eukaryotic translation initiation factor 1A (EIF1A), mRNA /cds=(207,641)	-1	ACAACCTCAAGTAAAGATGTCTCCA GTTTCTGAAGATAACGCACGCTGA
6338	Table 1	Hs.341573	BE646470	9970781	tc38c11.x1 cDNA, 3' end /clone=IMAGE:2066900 /clone_end=3'	-1	AAACACTCCACCTAAAGCAGGAAA GATGGCAATTCTAAATAGCAGCTA
6339	Table 1	Hs.88845	BE674685	10035307	AV733781 cDNA, 5' end /clone=cdAASF08 /clone_end=5'	-1	CGCCGCTCCTGGAGACCTGATAACTT AGGCTTGAATAATGACTTGTCT
6340	Table 1	Hs.181015	BE676054	10036595	signal transducer and activator of transcription 8, Interleukin-4 induced (STAT8), mRNA /cds=(165,2708)	-1	ATCCCATTTCTCCCTCTCAAGGCAGGG GTCATAGATCCTAAGCCATAAAAT
6341	Table 1	Hs.108327	BF001438	10701713	damage-specific DNA binding protein 1 (127kD) (DDB1), mRNA /cds=(109,3531)	-1	ACAGCATGAGAACTGTTAGTACGCA TACCTCAGTTCAAACCTTTAGGGA
6342	Table 1	NA	BF056055	10809951	7k07h12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443950 3' similar to contains element L1 repetitive eleme	-1	CACAATGCTGCCTCCTCTGTGGATGA CTGATGGCAAGAGTCTGAATTGAA
6343	Table 1	Hs.43857	BF058599	10812495	mRNA for KIAA1247 protein, partial cds /cds=(285,2942)	-1	TAAGAAATCCCAATTTTCAGGAGTGG TGGTGTCAATAAACGCTCTGTGGC
6344	Table 1	Hs.144583	BF059133	10813029	Homo sapiens, clone IMAGE:3462401, mRNA, partial cds /cds=(0,153)	-1	CGGCAGGGTGGCCTGTAACAATTTC A GTTTTCGAGAACATTCAGGTATT
6345	Table 1	Hs.144519	BF061421	10820331	T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6a2, mRNA /cds=(1767,2192)	-1	GCTGGAGGGAGAGGCACTGGGGAAT TTTTCTGGTGAATACTGAGGTAC

Table 8

6346	Table 1	Hs.96566	BF194880	11081165	602137338F1 cDNA, 5' end /clone=IMAGE:4274048 /clone_end=5'	-1	TGATACTTTGGTCTCTCTTCTGCTCA GGTCCCTTCATTTGTACTTTGGA
6347	Table 1	Hs.111583	BF197608	11088855	602365742F1 cDNA, 5' end /clone=IMAGE:4473923 /clone_end=5'	-1	ACTGCCAGTGAAGACTGTAAAGACAG AACACACTATTTTGGAGGGAGGAT
6348	Table 2	NA	BF197762	11087169	7p91f02.x1 NCI_CGAP_Skn1 cDNA clone IMAGE:3653139 3', mRNA sequence	-1	AGGAAGAGCCTGCACCTGTGGTGGA ACAATCAGGGAAAGGAAGTCAAAA
6349	Table 2	Hs.50785	BF221780	11128957	SEC22, vesicle trafficking protein (S. cerevisiae)-like 1 (SEC22L1), mRNA /cds=(119,766)	-1	TTTGGAGCTTCTATAGGAGTGGAGAG GGGCAGCTCATTGTTGAGAGTTGC
6350	Table 1	Hs.250811	BF432643	11444808	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA /cds=(170,790)	-1	TGATCTGACTGGAAAACAATCCTGTA TCCCCTCCCAAGAATCATGGGCT
6351	Table 1	Hs.293476	BF435621	11447923	hypothetical protein FKSG44 (FKSG44), mRNA /cds=(126,1520)	-1	CGTTTTCTGAGCATCCGTTGTGCCTT AACATTTTCTGCTTGCTCTTGGG
6352	Table 1	Hs.174104	BF445405	11510543	601438710F1 cDNA, 5' end /clone=IMAGE:3923643 /clone_end=5'	-1	ACTGCTGTTGCATGAATAGATGATAC AAAGCAAGTGATGATGTTGGTATG
6353	Table 1	Hs.295728	BF447885	11513023	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA /cds=(41,3187)	-1	AGTGAAAACCTGGTACAGTGTCTGCT TGATTTACAACATGTAACCTGTGA
6354	Table 1	Hs.181311	BF478238	11549065	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	-1	TGTCCTCTGAACCTGAGTGAAGAAAT ATACTCTGCTCTTGTACCTGCGT
6355	Table 1	Hs.179703	BF507849	11591147	tripartite motif protein 14 (TRIM14), mRNA /cds=(10,1230)	-1	CCATTTCACATCATGCTCTTCTCTAC CTTCCCTTCACAACCAATCAAGTG
6356	Table 1	Hs.300870	BF513602	11598781	mRNA; cDNA DKFZp547M072 (from clone DKFZp547M072) /cds=UNKNOWN	-1	AATACAGATTTCATTTTATTTAAGCGTC CGTGGCACCACAGGGACCCAG
6357	Table 1	Hs.283022	BF514341	11599520	triggering receptor expressed on myeloid cells 1 (TREM1), mRNA /cds=(47,751)	-1	GCCTCTTTTCTGATCACACAAGGG TCAGGATGGTGGAGTAAAGCTC
6358	Table 1	Hs.146085	BF591040	11683364	AL580165 cDNA /clone=CS0DJ005YB18-(3-prime)	-1	CTGGGGCCGTAGCAAAAATCATGAAA AACACTTCAACGTGCTCTTCAAT
6359	Table 1	Hs.170577	BF725383	12041294	602574255F1 cDNA, 5' end /clone=IMAGE:4702644 /clone_end=5'	-1	CAGACCTGTGGGCTGATTCCAGACT GAGAGTTGAAGTTTGTGTGATCA
6360	Table 1	Hs.104640	BF726114	12042025	HIV-1 inducer of short transcripts binding protein (FBI1), mRNA /cds=(0,1754)	-1	AAGGCAACCAACCACATTAGAAGTCT TGGCACTTTGTACCGAACGGGTA
6361	Table 1	Hs.296317	BF938959	12356279	mRNA for KIAA1789 protein, partial cds /cds=(3466,4899)	-1	GAAGTGACACTGACTGTATCTACCTC TCCTTTTCTTCATCAGGTGTCTCT
6362	Table 1	Hs.26136	BF940103	12357423	hypothetical protein MGC14156 (MGC14156), mRNA /cds=(82,426)	-1	AATTCCAAGGAGTGATGTTGGAATA GTCCCTCTAAGGGAGAGAAATGCA
6363	Table 1	Hs.133372	BF940291	12357611	AF150127 cDNA /clone=CBGBA01	-1	AGCCCCCTCCACCCACCCAGTACTTT TACAATGTGTTATTAAAGACCCCT
6364	Table 1	Hs.304900	BF980139	12347354	602288147F1 cDNA, 5' end /clone=IMAGE:4373963 /clone_end=5'	-1	CCATCCTTGAGAAATGTGGGCACCAA GTCCATAATCTCCATAAATCCAAT
6365	Table 1	Hs.8258	BG054968	12512220	cDNA FLJ14737 fis, clone NT2RP3002273, weakly similar to SCD6 PROTEIN /cds=(77,1468)	-1	TATGAGTTTATGCGTTTCCCAAGCCC TCCGAATCACTGACTGGGGCGTTT
6366	Table 1	Hs.5122	BG058599	12525258	602293015F1 cDNA, 5' end /clone=IMAGE:4387778 /clone_end=5'	-1	AGTTGGAGCTATCTGTGACAGCAGTTT CTCTACAGTTGTGCATAAATGTTT
6367	Table 2	Hs.89104	BG058739	12525527	602590917F1 cDNA, 5' end /clone=IMAGE:4717348 /clone_end=5'	-1	CGTGGGAGGATGACAAAGAAGCATG AGTCAACCCTGCTGGATAAACTAGA
6368	Table 1	Hs.166982	BG149747	12661777	phosphatidylinositol glycan, class F (PIGF), mRNA /cds=(67,726)	-1	GTGGTTTGGTCAGCATACACACTTCT CATTTTCATTTGATGTACACAGCCA
6369	Table 1	Hs.184456	BG230563	12725598	hypothetical protein (LOC51249), mRNA /cds=(0,611)	-1	GTGTGAAGTGACAGCCTTGTGTGTGA TGTTTTCTGCCTTCCCAAGTTTG
6370	Table 1	Hs.3353	BG236015	12749862	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA /cds=(175,1179)	-1	GTCTTCCCGCTTCTTCTCTCACCTA TGTAATTTCAAGTAGCTCTCAGC
6371	Table 1	Hs.83623	BG654774	13792183	nuclear receptor subfamily 1, group I, member 3 (NR1I3), mRNA /cds=(272,1318)	-1	TGTTTCGTAATTAATAGGTCTGGC CCAGAAGACCCACTCAATTGCCCT
6372	Table 1	Hs.109007	BG655723	13793132	602342214F1 cDNA, 5' end /clone=IMAGE:4452602 /clone_end=5'	-1	GTGGAATCAGCACACAACCAATG ACATTTAAGCACAGGATCATTATT
6373	Table 1	Hs.14453	BG744911	14055564	interferon consensus sequence binding protein 1 (ICSBP1), mRNA. /cds=(47,1327)	-1	AGAATGGCAGACCTGTTTGCTGAAGT GTTTCATAAGATAACAATAGGCTTG
6374	Table 1	Hs.2730	BI084548	14502878	heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA /cds=(28,1704)	-1	TGGGATTTTGTTTTAAAGTCATTTGGT TTGGGGAGGACCTTGTTTATTTT
6375	Table 1	Hs.298356	BI085832	14504162	mRNA; cDNA DKFZp434M162 (from clone DKFZp434M162) /cds=UNKNOWN	-1	TGGACAACTGACAGGGACTGCTTTG AAAGACAGGTAAGTGTGATAT

Table 8

6376	Table 1	Hs.132911	N20190	1125145	MR2-OT0079-290500-007-b03 cDNA	-1	AAGCCTGTTTTCACTCTAAAAATTCA AGAGGACACGCTAAGAACGATCA AGGTTCCCTTTCAAATAAAGATAAAG AATTTGACTTGGGACACTGCCAGA
6377	Table 1	Hs.334731	N58136	1202026	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds /cds=(0,2353)	-1	CTGTTCGAAAGTTGGAGACTGCCTGT ACCCAGGTTGATAGTCAATTGTTT AGCAGAGTTAAGTTTAAATTTCCATTC TCACTAGTTTGTGACCTTTGCCA
6378	Table 1	Hs.303018	N94511	1266820	zb80g04.s1 cDNA, 3' end /clone=IMAGE:309942 /clone_end=3'	-1	
6379	Table 1	NA	W68708	1377589	z35h04.s1 Soares_fetal_heart_NbHH19W cDNA clone IMAGE:342679 3', mRNA sequence	-1	
6380	Table 1	NA	W86427	1400194	zh61c11.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:416564 3', mRNA sequence	-1	TGAGTATTGTTGTGGGGCGGGTAT GTCTGTATATAAATCTGTGCAGCCA
6381	Table 3A	NA		36G5		1	CCCTTGACAGATACATGACAGGCA GGGGCTGGAGTCTTGTCCATCCTG GAGTAGTTGTCTTCTGGCACTAAC GTTGAGCTCGTGTACGCACTGAAG GAGTCCAATCTACACTCTAGTAGTA AGACAGAAGAGTTGGCATACGAGT GGCTGAACTTACTCATTAAAGCCACAT AACTTCGAGTCAAGTCCAGTCCA GCTCTCAAGCTCTCCCAATAAAGCT CTATCGGGAAACAAATGAACCACT
6382	Table 3A	NA		36F11		1	AGGAATGCACACATTGCTCCAGGATC ACTGTGAGGATTAAGGAGATGGT AGTAACGGAACAGTTCCAGTACTCC TGTTCTTAGTGTAGCAGGTGATG GGTGTGAACCATGAGAAGTTCGACAA CAGCCTCAAGATCATCAGCAATGA
6383	Table 1	NA		37G7		1	
6384	Table 1	NA		37G8		1	
6385	Table 3A	Hs.197345			thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846)	1	
6386	Table 1	NA		40E4		1	
6387	Table 3A	NA		41E9		1	
6388	Table 3A	Hs.169476			Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	1	
6389	Table 3A	NA		47E5		1	GGAGGTGTATAGGCTGGGATTTGAAA AGGAAAATAATCAGCGTGGTGCCA CCTAGACACCTGCATCAGTCAAGGTC ATGGATATTGGGAAGACAGACAGC TCCAGCAGATATAGGAAGCAGTGTAT CTAAACAGACAAATAAAAGGCCT ATCTAGTGTACGAGACTTGGAGTCAG GCAGTGAGACTGGTGGGGCACGGG
6390	Table 2	NA		47D11		1	
6391	Table 1	NA		50A11		1	
6392	Table 3A	Hs.132906			DNA sequence from clone RP11- 404F10 on chromosome 1q23.1-24.1. Contains the 5' end of the SLAM gene for signaling lymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated)) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene. Contains ESTs, STSs and GSSs /cds=(41,1048)	1	
6393	Table 1	NA		52B9		1	TGGTTTAATGGAAATGCTCTGGAAA ATTCTTTTGCAACAGTTCATCGCT CACTAAAGAGTGGGAGGTGCAGC ACCTGGCTGGGGAACAGAATATGG
6394	Table 1	NA		53B1		1	
6395	Table 1	NA		53E3		1	AAACGAATCAGCTGCCTCGAAAGGG ACATATATTGTTCTTTAAGCATTT AAGGGTTCAATTTCTCTTTGGAAGG TGATGGTAAGGGTGTGGCTCCAGA TGGACAATTCCAAGTCCAAGAGGACT GTCTACTTTCGACCTTGTGTGATT TTGTGTTAACCTGTTGTCCACGCTAA GATACAAACTTCCCGAGGAAAGT TGTCACAGTGTCTATTATTGCCCG GTTCTTAAAGTGAGAGCATCCTGA ACAATGATATTGATGAGGCACCCAGT CTTTTCATTACTCTGAGTGAAGT AGATCGAGATCTCAGTCTCTGCTT CATCTGTGAGCTTGCTTCAGTCA
6396	Table 1	NA		53E10		1	
6397	Table 2	NA		53G7		1	
6398	Table 1	NA		54F4		1	
6399	Table 1	NA		54G9		1	
6400	Table 1	NA		59G1		1	
6401	Table 1	Hs.48320			mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds /cds=(317,2833)	1	
6402	Table 1	NA		60G8		1	GGCCAGAGACCCTAAGCTGCTTAATA CATTTATACCACATCCTTCTCAGC CCCTTGGAAATTAATTTCAACTTCTT TCTTTCCCACTAGACGGGACTT CTTTGTAGATGCAGAGAGAAGCTATA AGAAACCCAGTACTTCCCGGGCG ACTGCCACATCTGACTTTACAGAATA ACCAATGTAAGTTAAATAGAGAAAC AG
6403	Table 2	NA		62C9		1	
6404	Table 3A	NA		62F11		1	
6405	Table 1	NA		63E1		1	

Table 8

6406	Table 2	NA	65B1	1	AGTCTTGCGAGTCAACTCAGACTCAA
6407	Table 2	NA	65D10	1	ATGTAGAACTGGGAAGGACAGTGC
6408	Table 2	NA	65D11	1	AGCACTGTGCAGATGGCTTTAGAAGA
6409	Table 2	NA	65D12	1	TTCAGAACAGAAAGCACAATCTGTT
6410	Table 1	NA	68C9	1	AGCACTGTGCAGATGGCTTTGGAAGA
6411	Table 1	NA	69F8	1	TTCAGAACAGAAAGCACAATCTGTT
6412	Table 1	NA	69H11	1	CTATGGAGTCTTGGAGGACACTGGA
6413	Table 3A	NA	70B6	1	GTCACCATGCTAACACTGTGCAGAT
6414	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA /cds=(139,930)	1	CCCTGTCCACCCTTCGTGGCCAGTGC
6415	Table 2	NA	72D4	1	CAGACAGTAACTAGTGGATGCTAAA
6416	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA /cds=(64,870)	1	GAGAGAATAGGGTAGAGAGACCGGG
6417	Table 2	NA	72D8	1	ACTTGGGTAGAGATGACCGGGATTTC
6418	Table 1	NA	73C4	1	AGTGGAAGCTAGGAGAAATATCGAAT
6419	Table 1	NA	73H4	1	GTGTTAGGGACTTTGAAGTTACCA
6420	Table 2	NA	73A7	1	CTGCATCTCTCTTTACTACCAGTGATT
6421	Table 3A	Hs.174228	small inducible cytokine subfamily C, member 2 (SCYC2), mRNA /cds=(0,344)	1	ACAAAGTGGGGTTTGGTGGGAGT
6422	Table 3A	Hs.3945	CGI-107 protein (LOC51012), mRNA /cds=(84,719)	1	TCTCTGACTTCTTATTACCAAGGACA
6423	Table 1	NA	75A2	1	CTCTATCTGTTGCCTCTTACTCTT
6424	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	1	CAGTTCCAGATGTGCGTGTGTGGGT
6425	Table 2	NA	75B12	1	CCCCAAGTATCACCTTCCAATTTC
6426	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	1	AACGACCCCTGTATTGCAGAAAGATTGT
6427	Table 3A	NA	101G7	1	AGACATTCTGTATGCCACAGATGA
6428	Table 3A	Hs.179565	minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA /cds=(44,2470)	1	ATTTACTCAAGTTTGTCCCTTGCC
6429	Table 1	Hs.119640	hBKL for basic kruppel like factor (LOC51274), mRNA /cds=(55,1092)	1	CACTGAAGCCAAACCACAGAAGACTT
6430	Table 3A	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA /cds=(280,1302)	1	TTGAGAATGAGGAGACAAATGAGT
6431	Table 1	NA	105A10	1	AGGTGAAAATTACTCTTCAGAAAGATA
6432	Table 1	NA	107G11	1	GCAGAGTGGATAATGGCCCATCGA
6433	Table 1	NA	107H8	1	TGCAGTGAGACTACATTTCTGTCTAA
6434	Table 3A	Hs.64239	DNA sequence from clone RP5- 1174N9 on chromosome 1p34.1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs, STSs, GSSs and two putative CpG islands /cds=(0,2195)	1	AGAAGATGTGTGAGTTCCGTCCTT
6435	Table 1	NA	109H9	1	TCCAGCCAGCCAGCTCATTTCACTTT
6436	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2667)	1	ACACCCTCATGGACTGGGATTATA
6437	Table 3A	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA /cds=(147,1736)	1	TTTCATACATTGGAAGTCCACCTGAC
				1	TTTGGACCAACCCAGAACAGAGC
				1	AGCACCGGAATACAAAATGATACTA
				1	TGCTGCCCTCCTAGATCTCAGGGA
				1	TGCCCATACATGAGTATTTGTCTA
				1	AAACATGTCTTCTTTGTAGCAGCT
				1	GCAAATCTAACTGCAGGAAAATTTT
				1	TGCACCCGAAGTATTCAGATCCCT
				1	GGCCCAAGTCTAATGTAACCAATGAT
				1	GCCATGTGCATATTGGAACCATA
				1	GGGGAAGAAACAAGATAATCTAGTGAC
				1	CTCACACAGTCTATGCCCAAGGCC
				1	AATTCAACTGAAGCGGAGGAATGTTG
				1	GTGATGAAGCTGAGATCAGGACTC
				1	CACCTATATCGAAAGTTTGGGCTCAT
				1	CTCCCATTTGGTGGCAAGACTCC
				1	TGGTGGAAGAGTGTGCTGTCTGCACA
				1	ATTACACTCAAGTTTACCTCTGGT
				1	ACGATAATACTGTTGGTTACTGCCAT
				1	AAATATTGGAAGCTAATGTAAAATGC
				1	A
				1	TTCTCTTATAAAGGACAGCAAGTTTAA
				1	AATGGAGCAAGGAGCATTGGAAA
				1	TGGCCAAAGAAATAGAAGCTCTAGACC
				1	TTCTTATTTCTATCGTGAAAACA
				1	ACATGACCTGTGCAGTGTGTGGCTGT
				1	GAATTCTGTTGGCTTTGTATGAAA
				1	TGACATAACTACCATCCCTGCAACTA
				1	ATGAACCCACCCTCACAGCTTCCT
				1	GAATGACATAAACCCCTCCGGTCTG
				1	AGGTCCGGCTTCAGGCTTGTCTC
				1	GCCTTTCTCACTCCATCCCCACCCAA
				1	AGTGCTCAGACCTTGTCTAGTTAT

Table 8

6438	Table 3A	Hs.333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5' 129A12	1	TCGTTTTACAACGTCGTGACTGGGAA AACCTGGCGTTACCCAACCTTAAT
6439	Table 1	NA		1	TGTTTTGTTTTCTGAAACGAAATCCTG CTCTGTTGGCCAGCTAGAACGC
6440	Table 1	NA	129F10	1	CAGAAGCTGGATGACGTTGCTCCATC TTCACCTGTGAATGAGACATGAT
6441	Table 3A	NA	137D4	1	CACATCTTCCATTGAGCCCTACCATG AAAACCGTACCTCGGGCGGACCA
6442	Table 1	NA	142F9	1	AATTTGCTTTAAATGAGTTTCCTTGC CATTGCACACTCCTATCTTTCTG
6443	Table 3A	Hs.250655	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(155,487)	1	CAGATGACACGCGCTCTCCACCAC CAACCCAAACCATGAGAATTTGCAA
6444	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	1	CCCATGCTGTTGATTGCTAAATGTAA CAGTCTGATCGTGACGCTGAATAA
6445	Table 1	NA	149G2	1	GACACAGACAGACCAAGCTATAGTCA GACCTGGTTACACACATACACACA
6446	Table 1	NA	149A11	1	TGGCAAAGATCACTGAAATTTAGGAC ACCAAAGCTAAACCCCAATGCT
6447	Table 3A	NA	151F11	1	GCTTGCTGCTCGAGACCGCTTGCTATA GAAACGCTGAGCTGCTGGTTTATG
6448	Table 1	NA	162E8	1	CTGGTTAAAGCCCACTTACTGACCT TCGCCGCCACACGCTTACTACTA
6449	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	1	GCATCCACCTCCTTCTCTCTCATG TGTGCTCTTCTTCTTCTACAGTA
6450	Table 1	NA	170F7	1	TTAAATCTATCAAGAATTCATCCAAAT TGGTACCCTGCCGGCCGCTCG
6451	Table 2	NA	170F9	1	AGTGCTGTATTGACTTTGCTCGGCAG TAGATGAAGCTATTCTGAACCCAA
6452	Table 3A	NA	177A3	1	TGCTGGACAAAGACAATGAGATGATT ATTGGTGGTGGGATGGCTGTTACC
6453	Table 1	NA	331A3	1	GTGGAAAAGTCACTACCGCTGGC AGGGAATGGGGCAATCTATTATAC
6454	Table 1	NA	331A5	1	AAGGGACAGGGAGCGGGCACAAAAT AAAACCTAGTTTGGTAGAAATTTATA
6455	Table 3A	NA	146C3	1	TCAAAGCACTGGAGATGAGAGCCAG GATGGACCCGAAAAGAATTTTACAG
6456	Table 1	NA	146D8	1	CAGGAACATGGCTGCAGCATATAAAA AGAATTGAATCCATACCTTTGTTAAC CCT
6457	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	1	TTGCCATAACCACGCTTGTAGATTAG TTCAATTTACTGACTTCAGATTGGG
6458	Table 1	NA	158G6	1	TTACAGGCAACCGGAGCATCCAATCA CCTTTCTCTAAGAGAGTACCTCGG
6459	Table 1	NA	158H8	1	AAAAGCATCTTCGAGAGGGACTGTCA ATTCTCGACTATTTTCCAACCCGC
6460	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(6,1217)	1	AAGAAGGAGCTTAATGCCAGGAACA GATTTTGCACTTGGTGGGTCTCAA
6461	Table 1	NA	158E9	1	AGAGACACCTAAATTACAGATTGTG AGCTGAGAGCTGGAGTTTTCATT
6462	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	1	AACAGCAAGAGAGATTACGAATTACG TTACTTCCAGATTAAACAGGACGA
6463	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	1	AGCGCAAGATAGATTTGGAATAGGAA TAAGCTCTAGTTCTTAAACAACCGA
6464	Table 3A	NA	155H10	1	GCATGGACAAGATGCCAAGGCCCGG ATGCTTTAGGATGAAGTCTTATCT
6465	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07028 /cds=UNKNOWN	1	CCTCCAGTCACCATACACAGGTTACC AGTGTGCAACTTGATGAAATCAGT
6466	Table 1	NA	159F6	1	CCAAACATCTGACTTGTGACTGTAA AAGGGAGGAGGTAGCCAATGATT
6467	Table 3A	NA	166F3	1	TTATGGTGGTCCGGGTGGGTGGTAG TTCAATGGGAGGTATGGGATTATT
6468	Table 1	NA	168F6	1	AGCTGTCTGGCTCAAAGATCTACATT CTGAAGTTGGCTGGAATGTCTTG
6469	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	1	CTGGTTCTTACCAGTGCCAGTGCCTT CAGGGCTTCACAGGCCAGTACCTC
6470	Table 2	Hs.25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	1	TGACACAGACTGTTTCAATCTTGGAG CAGCGACTGACTTTGACAGAAGAT
6471	Table 1	NA	168A9	1	TGCTATTTAAAGCACCATGATAAATAT GAGGCCACTTGGAAATCCATCCA
6472	Table 1	NA	171F11	1	GCAGGCGATGCTCTATAATCTAAAT GTATCTCTCTTCCCTAAGCTGAA
6473	Table 3A	NA	171G11	1	AAGTAAGACCACCTGTGAACCTGATC ATTATCTGGCGCACATAGGAAGAT
6474	Table 1	NA	175D1	1	GCTGGGGCTGGGAATTCGCTGGGCT AATGTGTCAATTTGACTTAAGAACT
6475	Table 1	NA	182H1	1	TTTGGGAAGAACCGATTGCTAAATTA TGCCTAATTCATGTCAAGAGAGGG

Table 8

6476	Table 3A	NA	184B5	1	AAGCAGTATACCATTATATAGCAAA
6477	Table 3A	NA	184D2	1	CAGCCAGTGGCCAGTTCAGTGAT
6478	Table 1	NA	184H1	1	CTGCCCTTTGGTAGTGAGAGGACCA
6479	Table 1	NA	48D1	1	CGCCAATGATGCTTTTAAGTAACCT
6480	Table 1	NA	98C1	1	CATTTCCTCATCTCTAAGGCACACTT
6481	Table 1	NA	98C3	1	GCTACCCCTCTTTGCTGACCCAG
6482	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	1	GCCTGCGTGTCTGCTCAGTGTTC
6483	Table 1	NA	98H4	1	TGGTCCTCCTCTAAGTACTCTAAA
6484	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2066)	1	AATCCTAGACATGTGCTTGTCAATGC
6485	Table 3A	NA	113F12	1	TCCCATGAAGGTAGTTTTCAAACA
6486	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	1	ACCAATAGAGAAGAAGCTCTAGAAGA
6487	Table 3A	NA	173A10	1	CAAAATCCCAAACCTTGGCACAAC
6488	Table 3A	Hs.334853	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	1	GGCTTCAACAGAACATCAATGCCA
6489	Table 3A	Hs.20252	DNA sequence from clone RP4- 646B12 on chromosome 1q42.11-42.3. Contains an FTH1 (ferritin, heavy polypeptide 1) (FTHL6) pseudogene, the gene for a novel Ras family protein, ESTs, STSs, GSSs and a putative CpG island /cds=(0,776)	1	AGACCAGTGAGAGCGTCAAAAA
6490	Table 1	NA	174D1	1	GCAAGCCCACTAAATAAACATCTAA
6491	Table 1	NA	45B9	1	CCAGCATCTTCCCCCATATAGG
6492	Table 1	NA	45H8	1	ATGGATCTGTTCTCTGTGCTAAATG
6493	Table 1	NA	111H6	1	TCTTGTGCGAGGTGTGTTTGTGG
6494	Table 1	NA	111E12	1	GCCGTAATGTCTCGGGATCTCTAATA
6495	Table 1	NA	111H11	1	ATAGAGGAGGTGAGTTGTGGTGTG
6496	Table 1	NA	112H3	1	AGGCACTCCTCAACCACTGTTCACCTG
6497	Table 1	NA	112E9	1	AATTCAACTGCTGAAATTGTAACA
6498	Table 1	NA	114G3	1	AGAGAGGGTTTTAAGGAGGGGCTTG
6499	Table 1	NA	117H6	1	TGAATACTTGGGAGAATACGGAAGG
6500	Table 1	NA	165E7	1	ATGAATTTGAAGACATGGTGGCTGAA
6501	Table 1	NA	165E11	1	AAGCGGCTCATCCAGATGGCTGT
6502	Table 1	NA	165F7	1	TTCCACAGATAGGTAAGCCAGGCGC
6503	Table 1	NA	176A6	1	GGCAAGATGAGACTGTATTCACTTA
6504	Table 1	NA	176G2	1	TCTTGTCTAGTCATTGTGGCAACCC
6505	Table 1	NA	176E10	1	CATCTGACACCTTGTGTAGTACCT
6508	Table 3A	NA	176F11	1	TTCTGGCAAGCTCTTGTCAATGGTGT
6507	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	1	CGACACTTCCTCTCTGTCTTCTGG
6508	Table 1	NA	71F2	1	TTTCAACATGGCTAGATCCATCAGAA
6509	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	1	ACTGAAGCGGGGAGAAAGCTCTC
				1	GGTACTCAAAGGAAATTAAGTCTTCT
				1	CTGGAACCTGGCAGAAAGTTT
				1	ATCCTTCTACCTTTTATTATGAAAGT
				1	TTTGGTACCTGGCCCGCGGAGCG
				1	ATTAAGGTTTTTAACATCTACTTTGGG
				1	TGATGGAGCCTTCAATGAAGTCA
				1	GAAAGACTACGAATTTGCTGGGAG
				1	GTAATAGGGAGCCTTCCACATAAA
				1	AAATGAGGTGAGCAATAACCTTGATT
				1	CGGTCTCCACTGGCAACATTTTA
				1	CTTCTCTCCCTGTAACCAAGCAGTGT
				1	GTGGGCGGGGCTCAGAACATATCT
				1	GTTGCCCTGATCTGGAAATCCTGTTG
				1	CTTCTTCTGGGATGAAGGAACCTC
				1	TAAGATAACCCACAGGCACCTTCTGT
				1	CATAAAGCCAACGACAGACAGCAG
				1	ATGGGAACAGGATGTTAAATACACAC
				1	ATACATACGCACACAAGCGTTGGG
				1	CCTCTGCTATCACTAGAGAAATGTAGA
				1	GAATGGAAATGGCTGCCTTTATGC
				1	GATACAGATGTGATTATTCAGCCTCA
				1	AGGGGACTTCTCCATTGCGTAACG
				1	TTATTGTTACCAATTAGAATCAGCAAT
				1	TCAACTGTGCGGTGATTTGGCCT
				1	TCATCACTTGGGTAACTAAAGGTTT
				1	GCGTATCACACAATTACACTACAA
				1	TTCATAGTCAAACAAAGGTAAGATC
				1	ATGCATATACCCACGGCAACAGG
				1	CCCACCCCTTCCCTCCATGTGAAG
				1	ATTTGGGTGCTTAACATATCATTT
				1	GGGAGACATGCTGATTCCACTCAAAG
				1	ATCTCATAATAACAGCTTTGGCC
				1	AAATAAATTGGAAATGGACATTGTG
				1	CTGTTTCACTTCAATGCTGTTAA

Table 8

6510	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA /cds=(85,2208) 124G4	1	AGAACAGTCTTGGGTTGAGGGGTGT GATGCCAGAATGTATTTTCGTACCT
6511	Table 1	NA		1	AAGGCCGAAGTCAATCCCATCTCCCTG AACCCAACTGCCAGTAGGTAGTTTC
6512	Table 1	NA	124C8	1	AGTTAAACTGTTGGTGAGGTAGTGTG TCAGGTACTCTGTATATTAGCTCT
6513	Table 1	NA	124F9	1	ACTGGATAAACAGAACGGATCAAAGA TAAAGTATTCTTGTTCCTGGGG
6514	Table 3A	NA	127A12	1	GTCCCTTAGGGGAGGAGAGTTGTC CTCTTGGCCACAGTCTACCCCTCAG
6515	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	1	ACTGGACTACTGAACTTTGAATACT GTCCTAAGGAAATAGGTCTGGGCA
6516	Table 1	NA	161E8	1	CAAAACAACAAAGTGGCCTCCATCGC TGTGAGCCTCTCAAGGGACAGGGC
6517	Table 1	NA	186E8	1	AAGGTGGCTGGCTTTTATGATACAGT GGTGGTAATGTAGCCCTTTTGGT
6518	Table 2	NA	191F6	1	TGCTCAATTGCCATACATGCATATA GGCCGGGATAGAAAATCGTCAGCT
6519	Table 3A	NA	193G3	1	TTCAAGGATGTGACTGATATCTGGTG TGGTTTATTTTGTGTTTGGGG
6520	Table 1	NA	194C2	1	AGCTTTGGAAATTTGAACAAGGTGGG GACAAATCAGGCAATAACAGACT
6521	db mining	NA	458C6	1	CACCTCCTGAGTGTTCCTGAGAACAA AAGGATCAGAGCTTCGGCTGTGAG
6522	Table 1	NA	458E4	1	TTTTCTTTTCGCTGACTTCCCACTC ACTGTCTGTCTCTCATTTCCTCT
6523	Table 1	NA	458G10	1	GCATGGGAATTGGCTGTCATCACTCA TAGCACGGGTATAACTCAAGGA
6524	Table 1	NA	459B3	1	GTCCACTCAAGTTACCTGGCTGTCTA TCITTTGGCTGACCCCTGAAGCGA
6525	Table 1	NA	459D2	1	CTAAGTAAGCAAGAGGCAGAGGGG AGGAGGGGAGTGTGTTGTTACTGTCC
6526	Table 1	NA	459E6	1	TGGTGGGTTGTCATGATTATTATGC AGGGTGAAGTTCACTATTGTTGTC
6527	Table 3A	Hs.20830	DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the homolog of the rat synaptic ras GTPase- activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS /cds=(163,2184)	1	AGCACATTGTGTCAGAAAGGTTTTCG AGGTATCTGAGGCACTGCTCACCT
6528	Table 3A	NA	460D5	1	AGAACAACACGGGATTGAAGTGGGA AGAGATGGGACCTCATTGGATCTG
6529	Table 1	NA	460B9	1	GAACAATAGACCTCTTCACTAGCTC CCTGCTGTTTGTGTTTGGTTGG
6530	Table 3A	NA	461A4	1	AGAGGATGACTTTGAGGTAATGTTT ACGATGCACGGTTTATAGGCGATGT
6531	Table 1	NA	461G6	1	GTGTCTGGGGAGTGAGGAGAGGTG GAGTAGACTCTGAGAGGAGTGAAAA
6532	Table 1	NA	461D9	1	AGATCATGTCTGGATTGTGTTTCCTA TTACCTAGAGACGAACACAGATCT
6533	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA /cds=(38,2455)	1	GTGTCCAGGACGAGCGGGAGTGCA CCATGGACCTCTCCGAGTTCATGAA
6534	Table 1	NA	461H7	1	TGTATGGCTTATAGCCAGAGATGAAA CAGAACCCCAAGTTAATATTGCCAG
6535	Table 1	Hs.333513	small inducible cytokine subfamily E, member 1 (endothelial monocyte- activating) (SCYE1), mRNA /cds=(49,987)	1	AGGTTTCAGAACTCTGGGCCCTACCTT TACAGGTTCAACAAAAGAAATGGCA
6536	Table 1	NA	463A5	1	AAGATGAGGCGTAGCTCATGTACAAA TGCAGCATTCTCATAAGTGCTTTA
6537	Table 1	NA	463B2	1	AGATAGTGGTATTTGGGTGCTGGGCT TGCTGAACTGAGGAGGTGGGTGC

Table 8

6538	Table 1	NA	463C5	1	CCTTGCAACCAGAGACGACTGACATAT
6539	Table 3A	Hs.40919	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(22,1272)	1	ATAGATGGGAGTCACTCATGCGCT
6540	Table 1	NA	463H5	1	GGTGTAGCGTGAAGATCTGGACAGC
6541	Table 1	NA	463A7	1	GCACTACGACCCGGGCCACTGTTTC
6542	Table 1	NA	463B10	1	AGAAGCAAACCTGTGAAGCTACTATC
6543	Table 1	NA	463C7	1	GTTTATCATCAGTGTGAATGCACT
6544	Table 1	NA	463F10	1	TAGTGATACAATTTGGGGTGCCAGAG
6545	Table 1	NA	464C2	1	GTTGGGGTAAGGAATTTTGAAGC
6546	Table 1	NA	464C5	1	GTGTGGCCTAAGGAACACCTCTTGTC
6547	Table 1	NA	464C10	1	GGGAGTAAGAGCCAGCCCTTCCTC
6548	Table 1	NA	464D8	1	AGATGCGGGCGCAAGCTTATGTCCT
6549	Table 1	Hs.221695	7k30d01.x1 cDNA, 3' end /clone=IMAGE:3476785 /clone_end=3'	1	GTTATGAGGGTTTAAATTAGATTGG
6550	Table 1	NA	464E7	1	TCATAACGCCCTTCAAAACATTGAAT
6551	Table 1	NA	464H12	1	AAAATCAGTGCAAAACATTGAGCA
6552	Table 2	NA	465B3	1	TGAGAAAAGGAGTTAGCAGAATATTAA
6553	Table 1	NA	465G2	1	CATACCGAGAAGCTGTTGTTAGCA
6554	Table 1	NA	465H5	1	CTGGAGACTCAGTCTGCTTAAGTGG
6555	Table 1	NA	465A12	1	AGGGGACGGGCACAGCCATTCTCC
6556	Table 1	NA	465F7	1	AAAGACCTGCCACTTATTTTGGCTC
6557	Table 1	NA	465G8	1	TCATCTGTACTCTTAAGTGTGTGT
6558	Table 1	NA	465H10	1	AGACACAGCTGCAGAAAACCTATTCT
6559	Table 3A	Hs.136309	DNA sequence from clone RP4- 612B15 on chromosome 1p22.2-31.1. Contains the (possibly pseudo) gene for a novel protein similar to 60S ribosomal protein L17 (RPL17), the gene for CGI- 61, endophilin B1 and KIAA0491, ESTs, STSs, GSSs and two CpG islands /cds=(1011,1406)	1	TTTCAAGCATGCACAGTCACAAAA
6560	Table 1	NA	515C12	1	CATTCAACAACACAAACCGACACCT
6561	Table 1	NA	515H10	1	ACTGTGTGCCACGCCACAGACAAG
6562	Table 1	NA	55G3	1	CCTAGGAAACACAGGTCAAAGAAACA
6563	Table 1	NA	55F9	1	CAGTCCAACATGTATTGAGAAATTC
6564	Table 3A	NA	99E7	1	AAACGCAATCTATTTAGGTTTGAGAT
6565	Table 1	Hs.319825	602021477F1 cDNA, 5' end /clone=IMAGE:4156915 /clone_end=5'	1	TAGAAGCTGAGGCCAAGGACTCA
6566	Table 1	Hs.17481	mRNA; cDNA DKFZp434G2415 (from clone DKFZp434G2415) /cds=UNKNOWN	1	TCCTCCAGATGCATGGTCCGTGAAGA
6567	Table 1	NA	116C9	1	AATTTAATAGCAAAGACGAGAAGA
6568	Table 1	NA	128F5	1	GGCTCTCATGCTTATGCCACACATCC
6569	Table 1	NA	135F10	1	TTGATTCTGCTTAGGAGTCTCTGG
6570	Table 1	NA	189F3	1	AAGCCTGAGCTAACAGAGCTGAGG
6571	Table 1	NA	189A8	1	ACAGTAGCTTATCTCTTTATGGG
6572	Table 1	NA	195H12	1	TGGATGATGGGATTGGATAAGCATGT
				1	GGACTGGATTGTGTACAAACTCT
				1	TGCTGTTTCTAGGATTACACGAAAT
				1	CATCACTTTGCCATATTTTGAAGCT
				1	GGCTCAGCACAAAGAGAAATTCGTAG
				1	CACTTTCATGTGAAAGCAGACCCA
				1	GATATTAAGGTACTTTCAGTACAAATC
				1	TGGTGCTGTGAGTGGGCTCATCC
				1	TCCAGTTTCTCATAAACAAATCTCTCT
				1	ATCCTGGCATTGGATTGGGTT
				1	TCATGGTCATAGCTGTAACCTGTGTG
				1	AAATAGTAATCAGATCAAAAAGCG
				1	ATATGTACCTGGAGGGCGGACGATC
				1	GAAATTACTAGTGAATTAGCGGCAG
				1	TGCGAGTGTAAATTTCTGTAAGGAGGG
				1	TATGGGATAATTAATAGCACGCCCT
				1	GCCCCCAGCATCAATTCATTTTGTA
				1	CCCTTAGTTTAAAGAACTTCTCCC
				1	AACTTTGCTTTCTGAAGGTTTTGGTG
				1	TACCTCGGGCGCGAACACGCTAAT
				1	ATTGACTCCACTTTGTGCCAAGCTCT
				1	GCGGGTAGGCATATTTTCATATCTT
				1	CAGTGGAGAAGCTGCACTGTCTCCG
				1	GGCTTGTTGATCCGATCTCTGTAC
				1	AGCTTTGAAAGTAATGTCTAACCCCTG
				1	CTGTCAGTTTATCACAAGTGCAAT
				1	AGCTTAATTGAATTGGAGGAGCACCG
				1	AACAGGCAGTTTCTGAGCAGTGG
				1	GCTCTCACTGATCTCTCTTCTATCT
				1	CTTTCTGCAGTTATACCAGCACT
				1	TGAGAAGAGCTGTGAAGGCAGAGGC
				1	GGGGCAAGTGCAAAGGCTCTGACTT
				1	AACTCCCTGTTTCAGTTTCAGTTGCTAA
				1	TGATCTCAAGCTCTTCCCTGATTA
				1	CAGCCTAATGCCCTAACACACAGATA
				1	CCATTGGTGGGCGAGTGACCCAG

Table 8

6573	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635)	1	CACCATCTTTTCTCGGATACTAGCC CGCAATACCCACTCACCTACCACC
6574	Table 3A	NA	466C4	1	AGGGTCTCCACCTTACAGAAGTACAT GAACAACCAAGAGATAGCAGGGCTG
6575	Table 1	NA	466D1	1	ACCAGGAAAAGTAAAAATCATAGTTG GTGTCTCTCGGGTTTCTCACCTTC
6576	Table 1	NA	466G2	1	ATGTATGAGAGAGATTGAGATGAGT TAAAGGAGGAAGGGAGGGTGGT
6577	Table 1	NA	466H5	1	CATGAGTATTGGCACTGGGGTTCAAG TTCCAGGGCAGAGCAGGATAAGAG
6578	Table 1	NA	466B7	1	CTCCTGGGGCTGGAGTCCCTGGTCTG CCTTCTGGGGCAGAGATTAGGTCTG
6579	Table 2	NA	466B10	1	TGGAACCTCAGTCAAAAACATCTGTA CTTTGTACAGGACAAAGATTGGC
6580	Table 1	NA	466C9	1	ATAGAACCTGTTTTACCTATGAGCCTT GCCTTGATTATTACTAGTGGC
6581	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	1	ACATCTCTTGTGAAAGTTCAAATGTTA CAGCAAGGTGTAAACACTCCACT
6582	Table 1	NA	121F1	1	GGGTGAATTAATCGGGAGATGGGTA GTCAGGGCAAATGATGGGTGGGTTT
6583	Table 1	NA	121A11	1	TGCAATTGTGGAGACAAATTGTTAGA GTTTAAATCCTGGCTCTGTCCCT
6584	Table 3A	NA	121F8	1	GGACCTATGTCCTCAAGACATGGAAA CTACTAGTTCTGTCGTGCCAGGAG
6585	Table 1	NA	178B2	1	AATTAAGGATGCCCTACCGACATCTA TCAGCATACCTGGAACAGGTTCTGA
6586	Table 3A	NA	178B5	1	CGGCCAACCAGGAGGGCAGGTGTT TTGGGCATCTGGTTTATAGTACCTC
6587	Table 1	NA	178F5	1	GCTGGGGTGAAGACTTGAAGACTCA GACCTCAGTGGAACAGATGAATGT
6588	Table 1	NA	178C12	1	CCCCAGGCTCTGTGACGCTTGAAATT CTAATTAGCGCAGAAAAGGGCTAA
6589	Table 1	NA	462A11	1	CCTGACTACGTGTTTTCCCCACAGAC ATCACACTGGTTCACCTCGTTGAA
6590	Table 1	Hs.13231	od15d12.s1 cDNA /cds=IMAGE:1368023	1	AATGGAAAGACACTTCTGTATACACT GGAAATCTCAGGAAATTTCTTTTCC
6591	Table 1	NA	462D9	1	GACAGTACAGTACCCTAAGAGCACTG AGGAGGGCCACCCACGTAACCTC
6592	Table 1	NA	462E8	1	TTTCCTTGGAGATTTCAGGCATCTTA GGCCGGGAAGGACCTCGAAGGTGG
6593	Table 1	NA	462F9	1	CTCCGCTTCTTTCACCTATTCTGTTAG TGTTTCTTTAAGCTTTGCCTTGT
6594	Table 1	NA	462F11	1	TCCACATTTTGTATCATGATTTATGAA AGCCCTGGGTTTGTATTGAGAA
6595	Table 1	NA	462G12	1	GCTATCTTCTGCTGAATCAGCGTAAT GCTGATATACACCTATTTTCTGT
6596	Table 1	NA	462H9	1	AAAAGAAAAGTTTTCAACCCAGGGA ATTTATAGTGGGTGTCAGTCGAGA
6597	Table 1	NA	472B1	1	AGGAGACGATGTAGGGGGAAGTGTG TTAGATTGTAATGGAGGGTTTGGG
6598	Table 1	NA	472C1	1	GCTCTTTCCAGACCCAGCCGCCAG GTTCTCTGTAGAGAAAATAAATGC
6599	Table 1	NA	472E6	1	AAGGAGGAATGGGAATCTCAAGCTCA AGGGCACTCTCACTAATTGTGGGT
6600	Table 1	NA	472F4	1	AAATAGCCACCTTCTCCCATTTTCT GTCAGAACACACACTTTATATCCA
6601	Table 1	NA	472G2	1	TTTGGTAAAAGAGATTGGAGGGGACA CCAGGGAAACAGGATTTTCTGGC
6602	Table 1	NA	472D7	1	AAGTGCTAAGGCATTCTCTAAACTAT CTTCCAGCTCCGGGCGACAATGG
6603	Table 1	NA	472G12	1	CCACTCTCTAAGTCAAGCGAGTCCCT CCTGCATACCTGTAAGTGGTCTG
6604	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	1	GGACTTTGCAGGCTTCATTCCTGTG TGTGTCTTTCTCTCTGGTGTGT
6605	Table 2	NA	64G9	1	ATTTGCTGGCCAATCCTGCTGACTAT GAATCTTTGGGGCACTGAGTTAC
6606	Table 1	NA	467E5	1	CTGGGGTACTGGGGAAAAGAACTG GTATTGAGATTTTATATTGGGGCG
6607	Table 1	NA	467A8	1	TTGAGTAAGGCTCAGAGTTGCAGATG AGGTGCAGAGAACATCTGTGACT
6608	Table 1	NA	467C9	1	GGTCAGAGAGAAATGGTAGCTGA AGAAGCAGGGCAGGAGGCTCTAAC
6609	Table 3A	NA	467F8	1	TTTCCGGTATATTCGTGTGGGTTGAC TTTTGTGTGTGTGGTTGGTGG
6610	Table 1	NA	468E8	1	GGATCTCTTGTCTCTCACCTGTGT GACAGACTACTAACAGCCCACTG

Table 8

6611	Table 1	NA	468B9	1	ACAGTGTGGGACAGAAGAGTGCTCA
6612	Table 1	NA	468E10	1	GTGATTAAATGCCTGATAATAGATT
6613	Table 1	NA	468F10	1	CTCTCTCGCAATTTACAACCGCTTTC
6614	Table 1	NA	468F11	1	AGTACCATTACCCGTCCTCCTCT
6615	Table 1	NA	468G12	1	CTTTGGGGAGTGGAGTTGTTAGAT
6616	Table 1	NA	468H11	1	GGGGAGAGAATCAGAACAAGGAGA
6617	Table 1	NA	469B6	1	CCTTACTGCTTACGGTCATCGGTCAT
6618	Table 1	NA	469D2	1	CAGCCCAACCCGCTTGGTTAGGTG
6619	Table 1	NA	469A10	1	AGAGTATAATTTCCCCAGTGTGGAGT
6620	Table 1	NA	469E12	1	GGTTAGTGTGCTAAAGAAGAGGT
6621	Table 1	NA	469F8	1	CTGATGTCGTGTCTGCACTCACCTGG
6622	Table 1	NA	469G8	1	TCATGTGTTCTGTTGTGCGGTAGT
6623	Table 1	NA	470B2	1	AGGGGCAGAGAAGAATCCACACTCA
6624	Table 1	Hs.118174	tetratricopeptide repeat domain 3	1	CAAGAGATGACCAAGGAGTAAACTG
6625	Table 1	NA	(TTC3), mRNA /cds=(2082,7460)	1	CCCAGCAGAGGCCAACAAGCAGCCA
			470C3	1	TACCCAAACTTCAGCCAAAATAAAA
				1	TGTGCAAAATACGGCGAGAAGAAGTG
				1	CATGAGAAAGTGCTTTATAAGCTGT
				1	CCAGCTTTTCCTTTGATGTTAGTTAG
				1	CAGTAAGTCACAGGTTTGAGCCCC
				1	GGCACGCATCCTCATTCTGCATGCT
				1	CTTAGAATATCTATCAATGATCAT
				1	ACTTCTATACTCAGTGCCTGTGGGT
				1	AACCAAGCAAGCAGGTTTGTGTCT
				1	CGGGGATGTGGGGAAGACAGACACT
				1	GCCTTAGAGCATGAATATTTGAAGA
				1	AGGTAGACTATTTAGCTGGAAGCATC
				1	CAAAACAGGGGATTTTAAAAATACTCA
				1	AAAATGTAGGTTAAAACTCTCACTTAA
					GAAGGAGAAGATCTGAGTAAACCCA
6626	Table 1	NA	470D5	1	ACCTGAACAATGAATGAAGAAAGGAA
6627	Table 1	NA	470E1	1	GACTTGGTTCTTCTAGCTCTGGAC
6628	Table 1	NA	470E5	1	CATGGCTCACAGCTCTAACACTCCC
6629	Table 1	NA	470F3	1	CTCCCTCCAGATCCTAAGAAGAAAG
6630	Table 1	NA	470G6	1	TCTGAGCTTCACTTCAAGAACTGGTA
6631	Table 1	NA	470B8	1	GTCCAAAAGAACTGGTTTCGTTTCA
6632	Table 1	NA	470G10	1	ACTTCACTCACTTTTAGCCTGTTTAT
6633	Table 1	NA	471D6	1	ATGAGCTTGTCACTGCTTTTGT
6634	Table 1	NA	471F1	1	TGAGGAGGATGGGAGGCGCACAGGC
6635	Table 1	NA	471F4	1	AATTTAGCTAGATATAGAAGAGAA
6636	Table 1	NA	471F6	1	AGCTGATTGGATTCTTGCCTTTTGC
6637	Table 1	NA	471E9	1	ATCGGTCTAATTTATCAAGTGTGT
6638	Table 1	NA	471E11	1	TCCATCCTTGGAGCTTGACAAGCAT
6639	Table 1	NA	471H11	1	TCACACTACTGGCTCACCTACTAT
6640	Table 1	NA	473E4	1	TAGCACTGTAGCCAGAGTCCCTGCTT
6641	Table 1	NA	473F3	1	GTACCAAGGAGCTGGGTGGTGGTT
6642	Table 1	NA	473E11	1	TGGATAGTCAGAAATACGTGTTTGT
6643	Table 1	NA	476C1	1	GGATTGGGGAGGGAGGGAGGAAA
6644	Table 1	NA	476D3	1	GCACTCCTGGAACCTTCTCACTAATT
6645	Table 1	NA	476F5	1	CGGGGACCACTTTTGTGAATGTTG
6646	Table 1	NA	476G3	1	TTGCTGCGGATGACCTGACTGAGCC
6647	Table 2	NA	476G4	1	CTGGGAGACTGTGCTATAATCTCTC
6648	Table 1	NA	476A10	1	AGAAGGAGGATCTGTTCTAACATCT
6649	Table 1	NA	476G8	1	GCGAGGGGAGGACAAAGCATTGAA
6650	Table 1	NA	476H10	1	CTTGCACTGAGTGAAGATGAACCTT
				1	TCTTTCCAGCCCTGAGAGAGGGA
				1	GTCTAGCTGGCAGGTGATGGATGAAT
				1	GGATGAGCTGGCAGACCAACAGAA
				1	TGCATGGAAATGTTTCGAGTACGGGG
				1	AAAAAAGGGAGGCCAAAACCTGTGT
				1	TTTTAAGGTGTGACTCAATTACAGG
				1	CATTCTGTATTTTTCGATTGGT
				1	ACCTTTGGGAGAAAGTCTTACAACCTA
				1	CATGAAATGCAGATTTATGGACTC
				1	GAAGGGACAGAACAATCAACTGTGA
				1	GAGATGGGAAGAAAACCTCAATGGA
				1	CTAGTTTGGGACTTTTCAATTGGGCAC
				1	GTGAATCCAGGAGGGCTGAATTTT
				1	GGCCCAAGATTGTAGACAGCATAAAAA
				1	TAATTTTGGGCTTTTCTGTAAAA
				1	CTGGGCTTCTGTGTGAGAAGCACC
				1	GCAGCCAAGAACCAACCACTGCAACT
				1	GAAGGGGATTTCGGTGATGGGGGAA
				1	GCCAAGGGACAAGGGAAAAAGGAAA
				1	AACCCAACCATGAAAAAGAAGAGCT
				1	CTGGACTACGGCCAGGCGTGGGAG
				1	TGGCTATTTGAGTTTCTCTTACATGA
				1	AATGCCTGGCAACGTACACTGGC
				1	TGAACCTCTGATTTCCGCCGAACTAG
				1	GAGGAAACACCCAAAAGAAGACGG

Table 8

6651	Table 2	NA	477E1	1	TTTGCTGGGACTAAATCAAACCTGC ACTGCAGAGCAGGTGAGGGTTCAT
6652	Table 1	NA	477E8	1	TGGAGAGTGTGTATTACCATTTTT TACATTGCATCACATTTTACCATCTAT ATCT
6653	Table 2	NA	477A11	1	TTTGAAGCCCCTCATAGAGAAGAGAC TGTACCATAAGAGAAGCCCACTCA
6654	Table 1	NA	477D9	1	AACTCTCAGTCCATGAGCTTGATTAC TCCATTGTACCATTTGGAAGCCCA
6655	Table 1	NA	477D10	1	GTGGGTAGCCATTAAAGTGGTCTGGC ACAGAAAGGGACAAGTAGCTTCAAG
6656	Table 2	NA	480A3	1	CTGGTGCTGAGTGGAGTCACAGTAA GGCTGTAGATGGAGCGCCCTGGGAA
6657	Table 1	NA	480B5	1	TTTTGATGTGACCACTGTCGTCATGGC GGGGGACAGGAGCTTAGGGGGAAT
6658	Table 1	NA	480D2	1	ATTATGCATGTGAGGGGACAACCTT TATTAACAGGAGGGGTGTGTCTT
6659	Table 1	NA	480E2	1	TGGTCATGTTTCCCTCTTACTCCAC GACAGTTTCATTATTGTAACCAAG
6660	Table 1	NA	480E3	1	TTCTGTTGGTTATATGAATGGCAGTT ATTGTCCTCCAGTGTGTGGGTCT
6661	Table 1	NA	480F3	1	AGTCCTGGCAACTTTACCTGGGAATT GTCTGTAATCTTTAAGCAGTGGCG
6662	Table 1	NA	480G4	1	AGGACTTATCTAGCTTTCACAGATTC AGAGTGCCTTCAACATCATTTGT
6663	Table 1	NA	480C8	1	TTTAACAGGCTTATCTAGGACATAGG CCCAAGAGGGAGGAGGAGGAAGGC
6664	Table 1	NA	480D9	1	CTCCAGGCCGAACGAGCTCCACTC TGGATTAAAGATCTGTCACTTGACA
6665	Table 1	NA	480E7	1	GCAGGACTTGTGGCAGGACTCAACG GGAGAGAAAGAGGCTGAAACATAAA
6666	Table 1	NA	480E11	1	AAGAACATCCCACTTTTCCGGTAGG CAAGTGTCAAGTCACCTGGACAAT
6667	Table 1	NA	480F8	1	TCTGTGGCTTGTGTGGGACCTGC GCCCTTTAAATTAGGGCATATTTTA
6668	Table 1	NA	487F11	1	GCGCTAAAAACCTGGTGATTAAATGA CAAAACAGAACGTGAGAGAGATTT
6669	Table 3A	NA	499G1	1	TCCTGCACACAACAATAAAGACAAG AATAAAGGGCCACCATCAGTAGC
6670	Table 1	NA	518F10	1	ATGTTGTTCAAATTAAACATCATACCA CATGGGGGCAGCTACCAATTTTT
6671	Table 3A	NA	524A12	1	TAATATGAAAAGCTGGAAGAAGATTA AGGGGTTGAGGAGACGTGCCGGGT
6672	Table 1	NA	526B9	1	GTTACCCTGACGAATGCAGTCCTCGT GTGGAATGTCTATGCCCTCTTGAG
6673	Table 1	NA	583B5	1	ACACCAGCAGTCATAGGGGAAAGGG GAATACAGTTAATTGGGTATTGTT
6674	Table 1	NA	583D6	1	ACTCCCTCCCATCTCTGGTCTTTAGT TGGAAAGCAAGCTTTCGGACAACGG
6675	Table 1	NA	583G8	1	TCCAACAAGGGTTACGGCAGAATTTA TGCGAAAGTCTTCTTTGGGCTAAA
6676	Table 3A	NA	584A1	1	TTGTTCTGCTCAGGCCAAGGATTGTT GTGTGCTCTGTATTGCTGCTTTG
6677	Table 1	NA	584D3	1	GGCCCGGCATGTCTCGTTTGTGAG TCCTCATCCAATCCATCTTCATAT
6678	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t	1	GTGGGTTTTAGACACCTGCAGCAAG AAGAAATACTGACTGACTAGGCAT
6679	Table 3A	NA	591H9	1	TTTAAAGAAAAATCTATTATCTTGA GCATGGATGGGGGAATGCCAAGG
6680	Table 3A	Hs.6179	DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDELR (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, the DDX17 gene for DEAD/H (Asp-Glu- Ala-Asp/His) box polypeptide 17 (72kD), ESTs, STSs, GSSs and six putative CpG islands /cds=(307,2259) 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'	1	CAGAAGAAACATGGCAAACCTGCTCTG TGCTTTCAAACCAAGTGTCCCC
6681	Table 1	Hs.44577		1	GTTACTTAAGATCAGTATGTGTGGTG CATATGTGATTTGACCATTCAGT
6682	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	GAGAATTTCCGCTGTATCTATGACAC CAAGGGTCGCTTTGCTGTACCTCG
6683	Table 1	NA	119F12	1	CTGGGTAAATACTACCAACTTTGAG AAGGTTGGTCTCTGCTCTTCTGTA
6684	Table 1	NA	119G10	1	GGAAAGACAGGTGAGTGTGCCACAA CTACCTAACACATCAGCAAATCTGG

Table 8

6685	Table 1	NA		485A6	1	GTCACCTTTAGCGAGCGGGAAAAACAAT GGCGGAAAGGGAAAAACCTGGAAG	
6688	Table 1	NA		485D5	1	CGATAAGCTGTGGTGTGGGAGTGA GAGATGTTACTTTGCGAATGTTCAA	
6687	Table 1	NA		489H9	1	AAAGGCTAGGTTTGCAGAAAGCCCTTC TAAACTATGCTTTGGTGGTTACT	
6688	Table 2	NA		494B11	1	CTGACCCTGCCGGGCGGAAGATAAA ACAAAAACGAGAAGAACAAGCAAGA	
6689	Table 1	NA		478E5	1	AAGATTGTAAAAATACATTTTAGGCTC AAGAGTTCAGGGGTTTCAGAGC	
6690	Table 1	NA		478G6	1	TGCAAGCTGGCACCTTCACGTTTATT TTTAAAGGGCTTCACATCAAAGAT	
6691	Table 3A	NA		478H3	1	AAACAAAGAAGGAAAAATGAAGAGGG GAAAAAGATGAACATCAGGCTGGGT	
6692	Table 1	NA		478C7	1	TCCAAAGGATGTTCTGGTGTTCAGC ATGATTTCTGGTGTAGCTTTTCT	
6693	Table 1	NA		478G8	1	TTTGTGGGTGCGTGAGAGGGGATTTA TACTCCTTGAGCCATATTTTGTGA	
6694	Table 1	NA		478H7	1	GGGTTCACAGCATGGGTGGAGGTAA GTAGTATTCTCATTGGTTGGTTAGT	
6695	Table 3A	NA		479B4	1	GACAGTGAGAAGAATATGGAGTAGA GTCCTTTTGGTCTTTGAGGCGGTCA	
6696	Table 1	NA		479D2	1	AACAGCTGAAGAACAAGAAGGTGAG CTCTGAATGCGTCAGGTGGTCATTG	
6697	Table 1	NA		479G2	1	GGCTGACCAGTACAGGCTTGGGAAT TTTATGGTTGGGTGGTTTCTACCAA	
6698	Table 1	NA		479G3	1	GGGGGAGCTATATTACTGATTAAC CACCATTTCCTTACCCAACTTATG	
6699	Table 1	NA		479G5	1	AAGCTTTGTATTATGAGGTACTGGGG CTCTGGGGGATATTGAGATGAGAA	
6700	Table 1	NA		479G6	1	AGTCCTGCTGAATCATTGGTTTATAG AAGACTATCTGGAGGGCCTGATAG	
6701	Table 1	NA		479H4	1	GGAGCTTCCAGTCTAATAGAAAAGAT GCACCTACGAATAGACTTTGGGTA	
6702	Table 1	NA		479H5	1	TCTGTGCTCTGTGGACCCGTCACCCT GAGCTCCTCAGTTGCTGAACCATC	
6703	Table 1	NA		479H6	1	TGCTGGCATGTGGATAGACTTTAGCA AATGGTAGTCATCTTCTAATTTCT	
6704	Table 1	NA		479G12	1	AATGGGAATCTTAAGGCCTCTCTGGA AAGGGTGTGAGGGGGTTCGAGGGGG	
6705	Table 1	NA		479H12	1	TGCATATTGTCACTGACTGGCTAGGG TCTCTAAATTTATGAAACCTTACA	
6706	Table 1	NA		482A5	1	GTCAGCAACTAAAAAGGGAGATATAT CTTAGAGAGACTGGAATAAGCAACTC	
6707	Table 3A	NA		483G5	1	GGAAGGACTCAAACCTGGCCATAAAG GCAATACGGCATGTTCAATACACCA	
6708	Table 1	NA		486C4	1	TTTGTGACTATGAAATAGTGGTCCT GGTTTTAACTCTTTGGGGTTCCCT	
6709	Table 1	NA		490F10	1	AATTATATTTTAGGCTGATGTGGGTG GTCTGTAATGCTCTCATTTACCAC	
6710	Table 1	NA		493C2	1	CTGTGTTTCTGTATGGTATTGCATTTG TCCCGCCTGTTGGGTTTGGTGG	
6711	Table 1	NA		58G4	1	TTCATGCTCATTAGGACATTGAACAA ATGGCAGAGTAAGAAAGTTTGGCC	
6712	Table 3A	Hs.169370		DNA sequence from PAC 66H14 on chromosome 8q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs /cds=(12,1706) 598H2	1	GGGAATGGACTCATATGCAAGATTGC TGACTTCGGATTGGCCCGATTGAT	
6713	Table 1	NA		598H2	1	CAACACATGGGACGGGAAGGAAATC CTTCGCTGTGATTTTGTAAAAATA	
6714	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	1	CAGCCACCTCCTCAGGTCAGACAAG CCCAGCACCCAAATACCATATCTG
6715	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element; mRNA	1	GGCTTCCCTATTACCTCCCAGCGAAA TTCGTAGTCTTTCTCTATGGAGTT
6716	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	1	TGCTGATGTGTTAGGTAGTTGTGGCA CACTCACCTGTCTTTCCTAAATGC
6717	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element; contains	1	TTCATGCTCAGCAAAACAACGTTTTA GGATGGTGAGAGAAGACAAAGTAA
6718	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	1	TATTAACCACTCACGGGAGCTCTCCA TGCAITTTGGTATTTTCGTCTGGGG

Table 8

6719	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09-(random)	1	TTACCTGCTTTGCATGCTCTCCATCG TCAAAGTCTTCTGGAACTTAGGC
6720	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11-(random)	1	CCCCACCCCAACACATACAAACGTTT CCCACCAATCGTTGAACCTGCAAAA
6721	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element, mRNA s	1	TTCAAGGTCCCAATACCCCACTAACT CGAAGGAAGAAATGGAATCTATT
6722	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT CATCGAACTCCAGAACACCGTCG
6723	Table 3A	Hs.232000	AW380881	6885540	UH-H10p-abh-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	1	TGCATGTATCCCGTAATTCAAATCC AATTTACAGCCACTGCTGAATAT
6724	Table 3A	Hs.325568	AW384988	6889647	602385081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	1	TACAGGAAATGAACTAGACGGGTG GGGGACACTAGAATGAAAACCACT
6725	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	1	AGTTTCTGCTTTCACTGACTGAGGCT TTGCTTTAACTCGGTGACTCCCAA
6726	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	1	TCCCACTTCAAGTTAAGCACCAGAACG AATCACTAATTTCTGGAGCAGCAAG
6727	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	1	CATGGATGGGGGCACTGGTGTCTTCT AGTGTGTGAGGAGCAGACGAGATG
6728	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	1	TCACCACAGATGGGAAGATCGTTTCC TGAAAACAGCTATAAATCACAGA
6729	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	CAGACGCTCCAGTCTGCGCCGAGGTT AGTGTGTTTATTAGACCTGAAATGA
6730	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	1	CCCTTTAGGCCTCTTGCCCGAACAGT GAACACTAATAGATATCTTAAGCT
6731	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	1	ATGGGGATCATGTTTATTTCTCTCTA TATAATGGGCCAGTGTGTCTCCA
6732	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	1	AGCTGTAGACCATAAGCCACCTTCAG GTAGTGGTTTGGGAAATCAAGCAA
6733	Table 3A	NA	BE086076	8476469	PM2-BT0872-130400-006-h09 BT0872 cDNA, mRNA sequence	1	TGTAATATGCTTGTCTTCTACCTG CCCCCAGCTCTTGAAGTGGTGAA
6734	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	1	GGAGGGTGTGGGGAAGCAAGAGA ACATTCGTGTTAGGGCAGAGAAGAA
6735	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	1	GCATCTCCAGCTTTCATAGTTACCCA ACTTGTAACCAAGATGTGCTG
6736	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	1	GGCCAGTGCCAGACGGTAGCTAGTT GGATGCTAAAGGTAGAAATTTAGATA
6737	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	1	GGCATTGTAGGTTGACACCAGCAAAG ACTCAGAGTGACTTGAGCATTGGA
6738	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	1	AGCCCATTTGGATATGGCCCATCTTT ACCTAATGGCTACTATAGTGAGGT
6739	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	1	AATCACAGCAGTAACCTCCAGTAGGA AAGATTCTCAAAGGAATAGTTCTT
6740	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	1	AATGGTCAGGCACAGGTAGAAATCAA GTCTGTATGTATGTTTACACAGA
6741	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor- HGSC project=TCBA cDNA clone T	1	TACCTGAAGGTGTAGAGAGTCCCG CATCCAGCAAGGCCAACAGCTCCAC
6742	Table 3A	Hs.11050	BE763412	10193336	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	1	CTGTGTTTTTCCCAAAGCAACAATTT AAACAAAGTGAGAGCCACTGACA
6743	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	GACTCCGAGCTCAAGTCAGTCTGTAC CCCCAACCCCTAACCCACTGCATC
6744	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	1	TGTAACCTGACTTTATGTACTCAAG TCTTGCCCTTACTGAGTGCCTGA
6745	Table 3A	NA	BF364413	11328438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	1	TCTCTCTAACCAAACTGTAATCTTCA GGACCAGCAAACTCAGCCCAAGG
6746	Table 3A	NA	BF373638	11335663	MRO-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	AACCTTGGTTAAATGGGTTAATAGA GGATTGGAACACTTTGTTTGTCTGT
6747	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	1	AGAAGCAACCTGTGAAGCTACTATC GTTTATCATCAGTGTGAATGCACT
6748	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	1	GGACTAACTCCACCTCCTCTGCTAC TCCAGCTGCTTCTTAATCAACT
6749	Table 3A	NA	BF758480	12108380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	AGTCTTCCACCAGCATAGGTATCAC ACAACCAGCTCTGTTTTACTCCTG
6750	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	TTAGCTGGTACACTTGTTCAGAGTTA CTGGGAGCCGGTAAGATAGTCAAC
6751	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	1	AGCGTGATGCTTCTCATGTCTGGTGA TTTTCTGTGAGACATCTTCAAGC
6752	Table 3A	NA	BF805164	12134153	QV1-CI0173-081100-456-f03 CI0173 cDNA, mRNA sequence	1	CAGGGTTAACAAGATATGGAATTCA ATTCTTTTATATGCTGCAGCCATGTT
6753	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	1	CCT TGTAATTGATTCCGCATAAACGGTC ATTACTGGCACCTATGGCAGCACC

Table 8

6754	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	1	GTGATCCACTTGGAGCTGCTACTGGT CCCATTGAGTCTATAGTACTTCA
6755	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	TGCCATGAAATCTCTATTAATCTCAG AAAGATCAAAGGAGGTCCCGTGT
6756	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCCACCTGGCAAATCCTCAAGTGTGA CCCTAGTCATCTTTCTCCTTTTGG
6757	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGAAGTAC AGTCCCCTCTTCAAAGAAGATGC
6758	Table 3A	NA	BF877979	12268109	MRO-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCTCCTCCCTGGGATGGCATAGA AGAGACTTTAAACCAAATGAGCC
6759	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTCTGCCTGCCAAGAAG ACACAGTGAGAGGTGTCCACAGTC
6760	Table 3A	NA	BF898285	12289744	QV1-MT0228-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTCCACTTATTTACGAAGCCAC TGCTGTGAAGCTCTGCACCCTGC
6761	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCACATCCAGGGACAGT CACAATGACCTACGGCTTTAGCTG
6762	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	1	GCAGGGCTACACCAAGTCCATTGATA TTTGGTCTGTAGGCTGCATTTCTGG
6763	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAATGCCCTCTCTCCTT CCTTTTCCAGACCTGGTTTAAA
6764	Table 3A	NA	BF926187	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	1	TCGCCATTTGGTAGTTCACAGTGAC TGCTCTTCTATTTCGAAGCCAC
6765	Table 3A	NA	BF928644	12326772	QV3-NT0216-081200-517-g03 NT0216 cDNA, mRNA sequence	1	GTAGATTACTATGAGACCAGCAGCCT CTGCTCCAGCCAGCTGTGGTGTG
6766	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	1	TTTCCTTTTTCGCTGACTTTCTCACTCA CTGTCTGTCTCTCATTTTCTCCA
6767	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	1	TGGTAAGTTCTGGCAGTGTGGAGAC AGGGGAATAATCTCAACAGTAGGT
6768	Table 3A	NA	U46388	1238904	HSU46388 Human pancreatic cancer cell line Patu 8988t cDNA clone xs425, mRNA sequence	1	CCATGGTGGTGCTTGACTTTTGCTTTG GGGCTTAATCCTAGTACTTTGG
6769	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	1	TCAGTGGGTGTTGGTTGTCCATTAGT TGAGACTTAGTTGTTGCTCTGGGA
6770	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	1	GGCTGGACAGCAGATGATCAAATCT CAATACTACATGCCCATCTCTGTGG
6771	Table 3A	NA		36G5		-1	CAGGATGGAACAAGACTCCAGCCCC TGCTGTCTCATGTATCTGCAAGGG
6772	Table 3A	NA		36F11		-1	CTTCAGTGCCTACACGAGCTCAACGT TAGTGCCAGGAAGACAACACTACTC
6773	Table 1	NA		37G7		-1	ACTCGTATGCCAATCTTCTGTCTTC ACTACTAGAGTGATAGATTGGACTC
6774	Table 1	NA		37G8		-1	TGGACTGGAACCTGACTCGAAGTTAT GTGGCTTAATGAGTAAGTTCAGCC
6775	Table 3A	Hs.197345		thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA /cds=(17,1846)		-1	ACTGGTTCAATTTGTTCCGATAGAG CTTTATTGGAGGAGGCTTGAGAGC
6776	Table 1	NA		40E4		-1	ACCATCTCCTTTAATCCTCACAGTGA TCCTGGAGCAATGTGTGCATTCTCT
6777	Table 3A	NA		41E9		-1	CATCACCTGCTCACCTAGGAACCAAGG AGTACTGGGAACCTGTTCCGTTACT
6778	Table 3A	Hs.169476		Homo sapiens, glyceraldehyde-3- phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)		-1	TCATTGCTGATGATCTTGAAGGCTGT GTGCAACTTCTCATGGTTCACACC
6779	Table 3A	NA		47E5		-1	TGGCACCACGCTGATTATTTTCTTTT CAATCCCAGCCTATACACCTCC
6780	Table 2	NA		47D11		-1	GCTGTCTGTCTTCCCAATATCCATGA CCTTGACTGATGCAGGTGTCTAGG
6781	Table 1	NA		50A11		-1	AGGCCTTTTATTTGTCTGTTTAGATA CACTGCTTCTATATCTGCTGGA
6782	Table 3A	Hs.132906		DNA sequence from clone RP11- 404F10 on chromosome 1q23.1-24.1. Contains the 5' end of the SLAM gene for signaling lymphocytic activation molecule, a SET (SET translocation (myeloid leukemia-associated)) protein pseudogene, the CD48 gene for CD48 antigen (B-cell membrane protein), the gene for a novel LY9 (lymphocyte antigen 9) like protein and the 5' end of the LY9 gene. Contains ESTs, STSs and GSSs /cds=(41,1048)		-1	CCCGTGCCCCCAGCTCACTGCC TGACTCCAAGTCTCGTACACTAGAT
6783	Table 1	NA		52B9		-1	AGCGATGAACTGTTGCAAAAGAAATTT TCCAGAGCAATTTCCATTAAACCA
6784	Table 1	NA		53B1		-1	CCATATTCTTGTTCCTCCAGCCAGGTG CTGCACCTCCCACTCTTTTAGTG
6785	Table 1	NA		53E3		-1	AAATGCTTAAAGGAACAATATATGTC CCTTCGAGGCACGTGATTCGTTT

Table 8

6786	Table 1	NA	53E10	-1	TCTGGAGCCACACCCCTTACCATCACC
6787	Table 2	NA	53G7	-1	TTCCAAAGAAGAAATTGAACCCTT
6788	Table 1	NA	54F4	-1	AATCACACAAGGTCGAAAGTAGACAG
6789	Table 1	NA	54G9	-1	TCCTCTTGGACTTGGAATTGTCCA
6790	Table 1	NA	59G1	-1	ACTTTCTCCGGGAAGTTGTATCTT
6791	Table 1	Hs.48320	mRNA for ring-IBR-ring domain containing protein Dorfin, complete cds (cds=(317,2833))	-1	AGCGTGGACAAACAGGTTAACACAA
6792	Table 1	NA	60G8	-1	TCAGGATGCTCTCACTTTAAGAACC
6793	Table 2	NA	62C9	-1	GGCAAATAATAGAACTGTGACA
6794	Table 3A	NA	62F11	-1	ACTTCACTCAGAGTAAATGAAAAGAC
6795	Table 1	NA	63E1	-1	TGGGTGCCTCATCAATATCATTGT
6796	Table 2	NA	65B1	-1	TGACTGAAGGCAAGCTCAGATGAA
6797	Table 2	NA	65D10	-1	GCAGAGGACTGAAGATCTCGATCT
6798	Table 2	NA	65D11	-1	GCTGAGAAGGATGTGGTATAAATGTA
6799	Table 2	NA	65D12	-1	TTAAGCAGCTTAGGGTCTCTGGCC
6800	Table 1	NA	68C9	-1	AAGTCCCCGTCTAGTGGGAAAGAAA
6801	Table 1	NA	69F8	-1	GAAGTTGAACAAGTAATCCAAGGG
6802	Table 1	NA	69H11	-1	CGCCCCGCAAGTACTGGGGTTTCTTA
6803	Table 3A	NA	70B6	-1	TAGCTTCTCTCTGCATCTACAAAG
6804	Table 3A	Hs.17109	integral membrane protein 2A (ITM2A), mRNA (cds=(139,930))	-1	CTGTTTCTCTATTTAACTTACATTGG
6805	Table 2	NA	72D4	-1	TTATTCTGTAAAGTCAGATGTGGCAG
6806	Table 3A	Hs.234279	microtubule-associated protein, RP/EB family, member 1 (MAPRE1), mRNA (cds=(64,870))	-1	GCACTGTCCTTCCAGTTCTACATTT
6807	Table 2	NA	72D8	-1	GAGTCTGAGTTGACTCGCAAGACT
6808	Table 1	NA	73C4	-1	AACAGATTGTGCTTCTGTCTGAATC
6809	Table 1	NA	73H4	-1	TTCTAAAGCCATCTGCACAGTGCT
6810	Table 2	NA	73A7	-1	AACAGATTGTGCTTCTGTCTGAATC
6811	Table 3A	Hs.174228	small inducible cytokine subfamily C, member 2 (SCYC2), mRNA (cds=(0,344))	-1	TTCCAAAGCCATCTGCACAGTGCT
6812	Table 3A	Hs.3945	CGI-107 protein (LOC51012), mRNA (cds=(84,719))	-1	ATCTGCACAGTGTAGCATGGTGACT
6813	Table 1	NA	75A2	-1	CCAGTGTCTCCAAGACTCCATAG
6814	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA (cds=(104,1222))	-1	TTTAGCATCCACTAGTTACTGTCTGG
6815	Table 2	NA	75B12	-1	CACTGGCCACGAAAGGGTGACAGGG
6816	Table 2	Hs.205442	601439889F1 cDNA, 5' end (clone=IMAGE:3924407 /clone_end=5')	-1	GAATCCCGGTCTCTACCCAAGTC
6817	Table 3A	NA	101G7	-1	CCGGTCTCTCTACCCTATTCTCTC
6818	Table 3A	Hs.179565	minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA (cds=(44,2470))	-1	TGGTAACCTCAAAGTCCCTAACCAT
6819	Table 1	Hs.119640	hBKLf for basic knuppel like factor (LOC51274), mRNA (cds=(55,1092))	-1	TCGATATTTCTCCTAGCTTCCACT
6820	Table 3A	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA (cds=(280,1302))	-1	CCAGTGTCTCCAAGACTCCATAG
6821	Table 1	NA	105A10	-1	TTTACATCCAGTCCATGAGGTTGTA
6822	Table 1	NA	107G11	-1	TCGATATTTCTCCTAGCTTCCACT

Table 8

6823	Table 1	NA	107H8	-1	TGTTTTACGATAGAAATAAGGAAGG TCTAGAGCTTCTATTCTTTGGCCA
6824	Table 3A	Hs.64239	DNA sequence from clone RP5- 1174N9 on chromosome 1p34.1-35.3. Contains the gene for a novel protein with IBR domain, a (pseudo?) gene for a novel protein similar to MT1E (metallothionein 1E (functional)), ESTs, STSs, GSSs and two putative CpG islands /cds=(0,2195)	-1	TTTCATACAAGCCACAGAATTTCAC AGCCACACACTGCACAGGTCACTGT
6825	Table 1	NA	109H9	-1	AGGAAGCTGTGAGGGTGGGTTTCATT AGTTGCAGGGATGGTAGTTATGTCA
6826	Table 3A	Hs.80261	enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related) (HEF1), mRNA /cds=(163,2667)	-1	GAGACAAGCTGGAAGGCCGACCTC AGACCGGAGGGGGTTTATGTCAATC
6827	Table 3A	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR), mRNA /cds=(147,1736)	-1	ATAACTAGACAAGGTCTGAGCACTTT GGGTGGGGATGGAGTGAGAAAGGC
6828	Table 3A	Hs.333114	AV713318 cDNA, 5' end /clone=DCAAAC09 /clone_end=5'	-1	ATTAAGTTGGGTAACGCCAGGGTTTT CCCAGTCACGACGTTGTAAACGA
6829	Table 1	NA	129A12	-1	GCGTTCTAGCTGGGCCAACAGAGCA GGATTTTCGTTTCAGAAAACAAAACA
6830	Table 1	NA	129F10	-1	ATCATGTCTCATTAAACAGAGTGAAGA TGGAGCAACGTCATCCAGCTTCTG
6831	Table 3A	NA	137D4	-1	TGGTCGCGCCCGAGGTACGGTTTTTC ATGGTAGGGCTGAATGGAAGATGTG
6832	Table 1	NA	142F9	-1	CAGAAAGATAGGAGTGTGCAATGGC AAGGAAACTCAATTTAAAGCAAAAT
6833	Table 3A	Hs.250655	Prothymosin, alpha (gene sequence 28)	-1	TTGCAAAATCTCATGGTTTGGGTGG GTGGTGGAGAGCGCGTGCATCTG
6834	Table 3A	Hs.249495	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), transcript variant 2, mRNA /cds=(104,1222)	-1	TTATTCAGCGTCACGATCAGACTGTT ACATTTAGCAATCAACAGCATGGG
6835	Table 1	NA	149G2	-1	TGTGTGTATGTGTGAACAGGTCTG ACTATAGCTTGGTCTGTCTGTGTC
6836	Table 1	NA	149A11	-1	AGCATTTGGGGTTTTAGCTTTGGTGT CCTAAATTCAGTGATCTTTGCCA
6837	Table 3A	NA	151F11	-1	CATAAACCAGCAGCTCAGCGTTTCTA TAGCAAGCGGTCTCGAGCACAGC
6838	Table 1	NA	162E8	-1	TAGTGATAGGCGTGGTGGCGCGAA GGTCAGTAATGGGGCTTTTAAACAG
6839	Table 3A	Hs.334330	calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA /cds=(123,581)	-1	TACTGTAGAAAAGAAAGAGCACACACA TGAGACAGAGAAGGAGGTGGATGC
6840	Table 1	NA	170F7	-1	CGAGGCGGCCCGGCAGGGTACCAAT TTGGATGAATTCCTGATAGATTAA
6841	Table 2	NA	170F9	-1	TTGGGTTCCAGATAGCTTCATCTACT GCCGAGCAAAGTCAATACAGCACT
6842	Table 3A	NA	177A3	-1	GGTAACAGCCATCCACCAACCAATAA TCATCTCATTGCTTTGTCCAGCA
6843	Table 1	NA	331A3	-1	GTATGAATAGATTGCCCATTCCTCG CCAGCCTGGTAGTGACTTTTCCAC
6844	Table 1	NA	331A5	-1	TATAATTTCTACCAAACTAAGTTTTAT TTTGTGCCGCTCCCTGTCCCTT
6845	Table 3A	NA	146C3	-1	CTGTAAAATCTTTTCGGGTCCATCC TGGCTCTCATCTCCAGTGCTTTGA
6846	Table 1	NA	146D8	-1	AGGGTTAAACAAAAGTATGGAATCAA TTCTTTTATATGCTGCAGCCATGTTCTG
6847	Table 3A	Hs.153	ribosomal protein L7 (RPL7), mRNA /cds=(10,756)	-1	CCCAATCTGAAGTCAGTAAATGAACT AATCTACAAGCGTGGTTATGGCAA
6848	Table 1	NA	158G6	-1	CCGAGGTACTCTCTTAGAGAAAGGTG ATTGGATGCTCCGGTTGCCGTGAA
6849	Table 1	NA	158H6	-1	GCGGGTTGGAATAAGTCGAGAATTG ACAGTCCCTCTCGAAGATGCTTTT
6850	Table 3A	Hs.119598	ribosomal protein L3 (RPL3), mRNA /cds=(8,1217)	-1	TTGAGACCCCACTCAAACTGTCAAACTCT GTTCTGGCATTAAAGCTCCTTCTT
6851	Table 1	NA	158G11	-1	AATGAAAACTCCAGCTCTCAGCTCA CAAACTGTGAATTTAGGTGTCTCT
6852	Table 3A	Hs.326249	ribosomal protein L22 (RPL22), mRNA /cds=(51,437)	-1	TCGTCCTGGTTAATCTGGAAGTAACG TAATTCGTAACCTCTTTGCTGTT
6853	Table 3A	Hs.297753	vimentin (VIM), mRNA /cds=(122,1522)	-1	TCGGTTGTTAAGAACTAGAGCTTATT CCTATTCCAAATCTATCTTGGCGCT
6854	Table 3A	NA	155H10	-1	AGATAAGAACTTCATCCTAAAGCATC CGGGCCTTGGCATCTTGCCATGC
6855	Table 3A	Hs.108124	cDNA: FLJ23088 fls, clone LNG07026 /cds=UNKNOWN	-1	ACTGATTTTCATCAAGTTCGACACTGG TAACCTGTGTATGGTGACTGGAGG
6856	Table 1	NA	159F8	-1	AATCATTGGCTACCTCCTCCCTTTT ACAGTCACAAGTCCAGATGTTTGG

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6857	Table 3A	NA	166F3	-1	AATAAATCCCATACCTCCCATTGAAC TACCACCCACCCCGACCACCATAA
6858	Table 1	NA	166F6	-1	CAAGACATTTCCAGCCCAAGTTCAGAA TGTAAGATCTTTGAGCCAGACAGCT
6859	Table 1	Hs.8121	Notch (Drosophila) homolog 2 (NOTCH2), mRNA /cds=(12,7427)	-1	GAGGTAAGTGGCCTGTGAAGCCCTGA AGGCACTGGCACTGGTAGGAACCAG
6860	Table 2	Hs.25130	cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 /cds=UNKNOWN	-1	ATCTTCTGTCAAAGTCAGTCGCTGCT CCAAGATTGAAACAGTCTGTGTCA
6861	Table 1	NA	168A9	-1	TGGATGGATTTCCAAGTGGCCTCATA TTTATCATGGTGCTTTAAATAGCA
6862	Table 1	NA	171F11	-1	TTCAAGCTTAGGGAAGAGAGATACAT TTTAGATTATAGAGCATCGCCTGC
6863	Table 3A	NA	171G11	-1	ATCTTCTATGTGCGCCAGATAATGA TCAAGTTCACAGGTGGTCTTACTT
6864	Table 1	NA	175D1	-1	AGTTTCTTAAGTCAAATGACACATTAG CCCACGCAATTCCCAGCCCCAGC
6865	Table 1	NA	182H1	-1	CCCTCTTCTGACATGAATTAGGCATA ATTTAGCAATCGGTTCTTCCCAA
6866	Table 3A	NA	184B5	-1	ATACAGTGAAGTGGCCACTGGCTGTT TGCTATATAAATGGTATACTGCTT
6867	Table 3A	NA	184D2	-1	AGGTTACTTAAAGCATCATTGGCGT GGTCCTCTCACTACCAAGGGCAG
6868	Table 1	NA	184H1	-1	CTGGGGTCAGCAAAGAGGGGTAGCA AGTGTGCCTTAGAGATGAAGAAATG
6869	Table 1	NA	46D1	-1	TTTAGAGTACTTAGAGGAGGACCAGG AAACACTGAGACAGACACGCAGGC.
6870	Table 1	NA	98C1	-1	TGTTTGAAAACTACCTTCATGGGAGC AATGACAAGCACATGTCTAGGATT
6871	Table 1	NA	98C3	-1	TTTGTGCCAAGGTTTGGGATTTTGTG TTCTAGAGCTTCTTCTCTATTGGT
6872	Table 2	Hs.205442	601439689F1 cDNA, 5' end /clone=IMAGE:3924407 /clone_end=5'	-1	TTTTTGACGCTCTCTCACTGGTCTTG GCATTTGATGTTCTGTGAAGCC
6873	Table 1	NA	98H4	-1	CCTATAATGGGGGAAAGATGCTGGTT AGATGTTTATTTTAGTGGGCTTGC
6874	Table 1	Hs.169363	GLE1 (yeast homolog)-like, RNA export mediator (GLE1L), mRNA /cds=(87,2068)	-1	CCACAAACACACCCTGCCACAAAGACA TTTAGCACAGAGGAACAGATCCAT
6875	Table 3A	NA	113F12	-1	GACACCACAACCTCACCTCCTTATTA TTAGAGATCCCGAGACATTACGGC
6876	Table 1	Hs.30212	thyroid receptor interacting protein 15 (TRIP15), mRNA /cds=(15,1346)	-1	TGTTACAATTTTCAGCAGTTGAATTCA GTGAACACTGGTTGAGGAGTGCTCT
6877	Table 3A	NA	173A10	-1	CCTTCGCTATTCTCCCAAGTATTCAC AAGCCCTCCCTTAAACCCCTCTCT
6878	Table 3A	Hs.334853	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	-1	ACAGCCATCTGGGATGAGCCGCTTTT CAGCCACCATGTCTTCAAATTCAT
6879	Table 3A	Hs.20252	DNA sequence from clone RP4- 646B12 on chromosome 1q42.11-42.3. Contains an FTH1 (ferritin, heavy polypeptide 1) (FTHL6) pseudogene, the gene for a novel Ras family protein, ESTs, STSs, GSSs and a putative CpG island /cds=(0,776)	-1	TAACCTGAATACAGTCTCATCTTGCCG. CGCCTGGCTTACCTATCTGTGGAA
6880	Table 1	NA	174D1	-1	AGGTACTACACAAGGTGTGAGATGG GGTTGCCACAATGACTAGGACAAGA
6881	Table 1	NA	45B9	-1	CCAAGAAGACAGAGGAAGTGTGCA ACACCATGACAAGAGCTTGCCAGAA
6882	Table 1	NA	45H8	-1	GAGAGCTTTCTCCCCGCCCTTCAGTTT CTGATGGATCTAGCCATGTTGAAA
6883	Table 1	NA	111H6	-1	TAAACCTTTCTGCCAGGGTTCCAGAG AAAGAGTAATTTCTCTTTGAGTACC
6884	Table 1	NA	111E12	-1	CGCTCGCCGGGCCAGGTACCAAAAC TTTCATAATAAAAGGTAGGAAGGAT
6885	Table 1	NA	111H11	-1	TGACTTCATTGAAGGCTCCATCACCC AAAGTAGATGTTAAAAACCTTAAT
6886	Table 1	NA	112H3	-1	TTTATGTGGAAGGCTTCCCTATTACC TCCCAGCGAAATTCGTAGTCTTTC
6887	Table 1	NA	112E9	-1	TAAATGTTGCCAGTGGAGGACCGAA TCAAGGTTATTGCTGACCTCATTT
6888	Table 1	NA	114G3	-1	AGATATGTTCTGAGCCCCGCCACAC ACTGCCTGGTTACAGGGAGAGAAG
6889	Table 1	NA	117H6	-1	GAGGTTCCCTTCATCCAGAAGAAGCA ACAGGATTTCCAGATCAGGGCAAC
6890	Table 1	NA	165E7	-1	CTGGTCTGTGTCGTTGGCTTTATGAC AGGAAGTGCTGTGGGTTATCTTA

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6891	Table 1	NA	165E11	-1	CCCAACGCTTGTGTGCGTATGTATGT GTGTATTTAACATCCTGTTCCCAT
6892	Table 1	NA	165F7	-1	GCATAAAGGCAGCCATTTCCATTCTC TACATTCTCTAGTGATAGCAGAGG
6893	Table 1	NA	176A6	-1	CGTTACGCAATGGAGAAGTCCCCTTG AGGCTGAATAATCACATCTGTATC
6894	Table 1	NA	176G2	-1	AGGCCAAATCACCGCACAGTTGAATT GCTGATTCTAATTGGTAACAATAA
6895	Table 1	NA	176E10	-1	TTGTAGTGTAATTGTGTATACGCAA ACCTTTAGTTAACCCAAAGTGATGA
6896	Table 3A	NA	176F11	-1	CCTTGTTGCCGTGGGTATATGCATGA TCTTACCTTTTGTGACTATGAA
6897	Table 1	Hs.232400	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	-1	AAATGATATGTTAAGCACCCAAATCTT CACATGGAGGGGAAGGGGGTGGG
6898	Table 1	NA	71F2	-1	GGCCAAAGCTGTTTATTATGAGATCT TTGAGTGAATCAGCATGTCTCCC
6899	Table 1	Hs.172028	a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA /cds=(469,2715)	-1	TTAACAGCATTGAAGGTGAAACAGCA CAATGTCCCATTCCAAATTTATTT
6900	Table 1	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein- associated) (SFPQ), mRNA /cds=(85,2208)	-1	AGGTACGAAAATACATTCTGGCATCA CACCCCTGAACCCCAAGACTGTTCT
6901	Table 1	NA	124G4	-1	GAACCTACCTACTGGCAGTTGGGTTCA GGGAGATGGGATTGACTTCGCCTT
6902	Table 1	NA	124C8	-1	AGAGCTAATATACAGAGTACCTGACA CACTACCTCACCAACAGTTTAACT
6903	Table 1	NA	124F9	-1	GCCAGGCAACAAGAATACTTTTATC TTTGATCCGTTCTGTTTATCCAGT
6904	Table 3A	NA	127A12	-1	CTGAGGGTAGACTGTGGGCAAAGAG GACAACTCTCCCTCCCTAAGGGAC
6905	Table 1	Hs.50180	601652275F1 cDNA, 5' end /clone=IMAGE:3935610 /clone_end=5'	-1	TGCCCAGACCTATTTCTTAGGACAG TATTCTAAAGTCAGTAGTCCAGT
6906	Table 1	NA	161E8	-1	GCCCTGTCCCTTGAGAGGCTCACAG CGATGGAGGCCACTTTTGTGTTTG
6907	Table 1	NA	186E8	-1	ACCAAAAAGGGCTACATTACCACCAC TGTATCATAAAAGCCAGCCACCTT
6908	Table 2	NA	191F6	-1	AGCTGACGATTTTCTATCCCGGCTA TAGTGATGTATGGCAATTGAGCA
6909	Table 3A	NA	193G3	-1	CCCCAAAACAAACAAATAAACACACA CCAGATATCAGTCACATCCTTGAA
6910	Table 1	NA	194C2	-1	AGTCTGTTATTGCCTGATTTTGTCCC CACCTTGTTCAAATTTCCAAAGCT
6911	db mining	NA	458C6	-1	CTCACAGCCGAAGCTCTGATCCTTTG TTCTCAGGAAACACTCAGGAAGTG
6912	Table 1	NA	458E4	-1	AGAGAAAATGAGAGACAGACAGTGA GTGGGAAAGTCAGCGAAAAGGAAAA
6913	Table 1	NA	458G10	-1	TCCTTGAGTTTATACCCGTGCTATG AGTGATGACAGCCAATTCCCATGC
6914	Table 1	NA	459B3	-1	TCGCTTCAGGGGTCAGCCAAAAGATA GACAGCCAGGTAACCTTGAGTGGAC
6915	Table 1	NA	459D2	-1	GGACAGTACCAACACTCCCTCCTC CCCTCTGCCTCTTGTCTACTTAG
6916	Table 1	NA	459E6	-1	GACCAAATCTGAACTTCCACCCTGC ATAATAATCATGAACACCGCACCA
6917	Table 3A	Hs.20830	DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an Intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the homolog of the rat synaptic ras GTPase- activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS /cds=(163,2184)	-1	AGGTGAGCAGTGCCTCAGATACCTG CAAACCTTTCTGCACAAATGTGCT
6918	Table 3A	NA	460D5	-1	CAGATCCAATGAGGGTCCCATCTCTT CCCACTTCAATCCCGTGTGTTCT

Table 8

6919	Table 1	NA	460B9	-1	CCAACCAAACCATCAAACAGCAGGGA
6920	Table 3A	NA	461A4	-1	GCTAGTGAAGAGGTCTATTGTTCC
6921	Table 1	NA	461G6	-1	ACATCGCCTAAAACCGTCATCGTAA
6922	Table 1	NA	461D9	-1	ACATTTACCTCAAAGTCATCCTCT
6923	Table 3A	Hs.80768	chloride channel 7 (CLCN7), mRNA	-1	TTTTCACTCCTCTCAGAGTCTACTCC
6924	Table 1	NA	461H7	-1	ACCTCTCCTCACTCCCAGGACAC
6925	Table 1	Hs.333513	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA	-1	AGATCTGTGTTTCTCTAGGTAATA
6926	Table 1	NA	463A5	-1	GGAAACACAATCCAGACATGATCT
6927	Table 1	NA	463B2	-1	TTCATGAACCTCGAGAGGTCCATGGT
6928	Table 1	NA	463C5	-1	GCACCTCCCGCTCGTCTGGGACAC
6929	Table 3A	Hs.40919	hypothetical protein FLJ14511 (FLJ14511), mRNA	-1	CTGGCAATATTAACTTGGGTTCTGTT
6930	Table 1	NA	463H5	-1	TCATCTCTGGCTATAAGCCATACA
6931	Table 1	NA	463A7	-1	TGCCATTCTTTTGTGAACCTGTAAA
6932	Table 1	NA	463B10	-1	GGTAAGGCCAGATTCTGAAACCT
6933	Table 1	NA	463C7	-1	TAAAGCACTTATGAGAATGCTGCATT
6934	Table 1	NA	463F10	-1	TGTACATGAGCTACGCCTCATCTT
6935	Table 1	NA	464C2	-1	GCACCCAGCTCCTCAGTTCAGACAAG
6936	Table 1	NA	464C5	-1	CCCAGCACCCCAAATACCACTATCT
6937	Table 1	NA	464C10	-1	AGCGCATGAGTGACTCCCATCTATAT
6938	Table 1	NA	464D8	-1	ATGTCAGTCGTCTCTGGTGCAAGG
6939	Table 1	Hs.221695	7k30d01.x1 cDNA, 3' end	-1	GAAACAGTGGCCCGGTCGTAGTGC
6940	Table 1	NA	464E7	-1	GCTGTCCAGATCTTCACGCTACACC
6941	Table 1	NA	464H12	-1	AGTGCAATTCACACTGATGATAACGA
6942	Table 2	NA	465B3	-1	TAGTAGCTTCACAGGTTTGCTTCT
6943	Table 1	NA	465G2	-1	GCTTCAAAATTCCTTACCCCAACCT
6944	Table 1	NA	465H5	-1	CTGGCACCCCAAATTGATCACTA
6945	Table 1	NA	465A12	-1	GAGGAAGGGCTGGCTCTTACTCCCC
6946	Table 1	NA	465F7	-1	ACAAGAGGTGTTCTTAGGCCACAC
6947	Table 1	NA	465G8	-1	CCAATCTAATTTAAACCCCTACAACAG
6948	Table 1	NA	465H10	-1	GACATAAGCTTGCGCCCGCATCT
6949	Table 3A	Hs.136309	DNA sequence from clone RP4, 812B15 on chromosome 1p22.2-31.1. Contains the (possibly pseudo) gene for a novel protein similar to 60S ribosomal protein L17 (RPL17), the gene for CGI-61, endophilin B1 and KIAA0491, ESTs, STSs, GSSs and two CpG islands	-1	TGCTCAATGTTTTGCACTGATTTTATT
6950	Table 1	NA	515C12	-1	CAATGTTTTGAAGGGCGTTATGA
6951	Table 1	NA	515H10	-1	TGCTAACACAGCTTCTCGGTATGTT
6952	Table 1	NA	55G3	-1	AATATTCTGCTAACTCCTTTCTCA
6953	Table 1	NA	55F9	-1	GGAGGAATGGCTGTGCCCGTCCCCCT
6954	Table 3A	NA	99E7	-1	CCACTTAAGCGACCTGAGTCTCCAG
				-1	ACACACACTTAAGAGTACAGATGAGA
				-1	GCCAAAAATAAGTGGCAGGTCTTT
				-1	TTTTGTGACTGTGCATGCTTGAAAG
				-1	AATAAGTTTTCTGCAGCTGTGTCT
				-1	CTTGTCTGTGGCGTGGCACACAGTA
				-1	GGTGCTCGGTTTGTGTTGTTGAATG
				-1	GAATTCGAATACATGTTGGACTGTG
				-1	TTTCTTTGACCTGTGTTTCTTAGG
				-1	TGAGTCCTTGGCCTCAGCTTCTAATC
				-1	TCAAACCTAAATAGATTGCGTTT
				-1	TCITCTCGCTTTTGCTATTAAATTTCT
				-1	TCACGGACCATGCATCTGGAGGA
				-1	CCAGAGACTCCTAAGCAGAATCAAGG
				-1	ATGTGTGGCATAAGCATGAGAGCC
				-1	CCCATAAGAGGAATAAGCTACTGTC
				-1	CTCAGCTCTTGTTAGCTCAGGCTT
				-1	AGAGTTTGTAACACAATCCAGTCCAC
				-1	ATGCTTATCCAATCCCATCATCCA
				-1	AGCTCAAAATATGGCAAAGTGATGAT
				-1	TTCTGTGTTAATCCTAGAAACAGCA
				-1	TGGGTCTGCTTTCACATGAAAGTGCT
				-1	ACGAATTCCTCTTTGTGCTGAGCC
				-1	GGATGAGCCCACTCACAGCACCAGA
				-1	TTTGTACTGAAAGTACCTTAATATC
				-1	AACCCAAATCCAAATGCCAGGATAGA
				-1	AGAATTTGTTTATGAGAACTGGA
				-1	CGCTTTTGTATCTGATTACTATTTAC
				-1	ACAGGTTACAGCTATGACCATGA
				-1	CTGCCGCTAATTCAGTAGTAATTCG
				-1	ATCGTCCGCCCTCCAGGTACATAT
				-1	AGGCGTGCTATTAAATATCCCATACC
				-1	CTCCTTACAGAAATTACACTCGCA
				-1	GGGAGAAAGTTCTTTAACTAAGGGTA
				-1	CAAAATGAATTGAATGCTGGGGGC
				-1	ATTAGCGTGTTCGGCCCCGAGGTAC
				-1	ACCAAACCTTCAGAAAGCAAAGTT

Table 8

6955	Table 1	Hs.319825	103C4	-1	AAGATATGAAATATGCCTACCCGCAG AGCTTGGCACAAGTGGAGTCAAT
6956	Table 1	Hs.17481	mRNA; cDNA DKFZp434G2415 (from clone DKFZp434G2415) /cds=UNKNOWN	-1	GTACAGAGATCGGATCACACAAGCC CGGAGACAGTGCAGCTTCTCCACTG
6957	Table 1	NA	116C9	-1	AATGCACCTTGTGATAAACTGACAGCA GGGTTAGACATTACTTTCAAAGCT
6958	Table 1	NA	128F5	-1	CCACTGCTCAGGAACTGCCTGTTCCG GTGCTCCTCCAATTCAATTAAGCT
6959	Table 1	NA	135F10	-1	AGTGCTGGTATAACTGCAGAAAGAGA TAGAGAAGAGAGATCAGTGAGAGC
6960	Table 1	NA	189F3	-1	AAGTCAGGACCTTTGCACTTGCCCCG CCTCTGCCITTCACAGCTCTTCTCA
6961	Table 1	NA	189A8	-1	TAATCAGGGAAGAGCTTGAGATCATT AGCAACTGAACTGAACAGGGAGTT
6962	Table 1	NA	195H12	-1	CTGGGTACAGTCGCCCAATGGT ATCTGTGTGGTTAGGCATTAGGCTG
6963	Table 1	Hs.292457	Homo sapiens, clone MGC:16362 IMAGE:3927795, mRNA, complete cds /cds=(498,635)	-1	GGTGGTAGGTGAGTGGGTATTGCCG GCTAGTATCCGAGCAAAAGATGGTG
6964	Table 3A	NA	466C4	-1	CAGCCCTGCTATCTCTGGTTGTTTCAT. GTACTTCTGTAAGGTGGAGACCCT
6965	Table 1	NA	466D1	-1	GAAGGTGAGAAACCCGAGAGACACC AACTATGATTTTTACTTTTCTGGT
6966	Table 1	NA	466G2	-1	ACCACCCCTCCCTTCCCTCTTTAAC TCATCTCGAATCTCTCTCATACAT
6967	Table 1	NA	466H5	-1	CTCTTATCCTGCTCTGCCCTGGAAC TGAACCCAGTGCCCAATACTCATG
6968	Table 1	NA	466B7	-1	CGACCTAATCTCTGTCCCAAGAGGC AGACCAGGACTCCAGCCCAGGAG
6969	Table 2	NA	466B10	-1	GCCAAATCTTTGCTGTACAAAGTA CAGATGTTTTGACTGAAGTTCCA
6970	Table 1	NA	466C9	-1	GCCACAGTGAATAATACAAGGCAAG GCTCATAGGTAACCAAGTTCTAT
6971	Table 1	Hs.7187	mRNA for KIAA1757 protein, partial cds /cds=(347,4576)	-1	AGTGGAGTGTTACACCTTGCTGTAA CATTGGAATTTACAGAGATGT
6972	Table 1	NA	121F1	-1	AAACCCACCCATCATTTGCCCTGACT ACCCATCTCCCGATTAATTCACCC
6973	Table 1	NA	121A11	-1	AGGGAACAGAGCCAGGATTTAACTC TAACAATTTGTCTCCACAATTGCA
6974	Table 3A	NA	121F8	-1	CTCCTGGCAGCAGAACTAGTAGTT TCCATGTCTTGAGGACATAGGTCC
6975	Table 1	NA	178B2	-1	TCGAACCTGTTCCAGGTATGCTGATA GATGTCGGTAGGGCATCTTAATT
6976	Table 3A	NA	178B5	-1	GAGGTACTATAAACAGATGCCCAAA ACACCTGCCCTCCTGGGTTGGCCG
6977	Table 1	NA	178F5	-1	ACATTCTCTGTTTCCACTGAGGTCT GAGTCTTCAAGTTTCAACCCAGC
6978	Table 1	NA	178C12	-1	TTAGCCCTTTTCTGCGCTAATTAGAAT TTCAAGCGTCACAGAGCCTGGGG
6979	Table 1	NA	462A11	-1	TTCAACGAGGTGAACCAAGTGATGT CTGTGGGGGAAACAGTATGTCAGG
6980	Table 1	Hs.13231	od15d12.s1 cDNA /clone=IMAGE:1368023	-1	GGAAAAAGAAATTTCTGAGATTTTC CAGTGTATACAGAAAGTGCTTTCCAT
6981	Table 1	NA	462D9	-1	GAGTTCAGTGCGGGTGCCCTCCTC AGTGCTCTTAGGGTACTGTACTGTC
6982	Table 1	NA	462E8	-1	CCACCTTCGAGGTCCCTTCCGGCCTA AGATGCCTGAAATCTCCAAGGAAA
6983	Table 1	NA	462F9	-1	ACAAGGCCAAGCTTAAAGAAACACTA AACGAATGAGTGAAAGAAGCGGAG
6984	Table 1	NA	462F11	-1	TTCTCAATAACAACCCAGGGCTTTC ATAAATGCATGATCAAAATGTGGA
6985	Table 1	NA	462G12	-1	ACAGAAAATAGGGTGATATCAGCAT. TACGCTGATTACAGCAGAAGATAGC
6986	Table 1	NA	462H9	-1	TCTCGACTGACACCCACTATAAATTC CCTGGGTTGAAAACTTTTCTTTT
6987	Table 1	NA	472B1	-1	TCCAAACCCCTCCATTACAATCTAAC ACACTTCCCTTACATCGTCTCCT
6988	Table 1	NA	472C1	-1	GCATTTATTTTCTTCTACAGAGAACCT GGCGGCTGGGTCTGGGAAAGAGC
6989	Table 1	NA	472E6	-1	ACCACAATTAGTGAGAGTGCCCTTG AGCTTGAGATTCCCAATTCCTCTT
6990	Table 1	NA	472F4	-1	TGGATATAAAGTGTGTTCTGACAG AAAATGGGGAGAAGGTGGCTATTT
6991	Table 1	NA	472G2	-1	GCCAGAAAATCCTGGTTTCCCTGGTG TCCCTCCAATCTCTTTTACCAA
6992	Table 1	NA	472D7	-1	CCATTGTGCCCCGGAGCTGGAAGA TAGTTTAGAGAATGCCCTTAGCACTT
6993	Table 1	NA	472G12	-1	CAGCACCCAGTACAGGTATGCAGGA AGGACTCGCTTACTTAGAGAGTGG

Table 8

6994	Table 1	Hs.75354	mRNA for KIAA0219 gene, partial cds /cds=(0,7239)	-1	AACACACCAGAAGGAAAAAGACACAGA CAGGGAATGAAGCCTGCAAAAGTCC
6995	Table 2	NA	64G9	-1	GTAAGTCAGTGCCCCAAAGATTCAT AGTCAGCAGGATTGGCCAGCAAAT
6996	Table 1	NA	467E5	-1	CGCCCCAAATATAAAATCTCAATACC AGTTCCCTTTCCCCAGTACCCAG
6997	Table 1	NA	467A8	-1	AGTCACAGGATGTTCTCTGCACCTCA TCTGCAACTCTGAGCCTTACTCAA
6998	Table 1	NA	467C9	-1	GTTAGAGCCCTCGTGCCCTGCTTCTT CAGCTACCATTTCTCTCTGTGACC
6999	Table 3A	NA	467F8	-1	CCACCACAACACACACAAAAAGT CAACCACACGAATATACCGGAAA
7000	Table 1	NA	468E6	-1	CAGTTGGGCTGTTAGTAGTCTGTAC ACAGGTGAGAGGAGCAAGAGATCC
7001	Table 1	NA	468B9	-1	AATCTATTATCAGGCATTTAATCACTG AGCACTCTTCTGTCCACACTGT
7002	Table 1	NA	468E10	-1	AGAGGAGTGACGGTGAATGGTACTG AAAGCGGTGTAAATGGCAGAGAG
7003	Table 1	NA	468F10	-1	TCTCCTTGTCTCTGATTCTCTCCCATC TACAACAACCTCCACTCCCCAAG
7004	Table 1	NA	468F11	-1	CACCTAACCAAGCGGGTGGGGCTGA TGACCGATGACCGTAAGCAGTAAGG
7005	Table 1	NA	468G12	-1	ACCTCTTCTTTAGCAACACTAACCAC TCCACACTGGGGAAATATACTCT
7006	Table 1	NA	468H11	-1	ACTACCGCACACAGAACACATGACC AGGTGAGTGACAGACACGACATCAG
7007	Table 1	NA	469B6	-1	CAGTTTTACTCTCTGGTCATCTCTTGT GAGTGTGGATTCTCTCTGCCCT
7008	Table 1	NA	469D2	-1	TTTTATTTGGCTGAAGTTGGGTATG GCTGCTTGTGGCTCTGCTGGG
7009	Table 1	NA	469A10	-1	ACAGCTTATAAAGCACTTTCTCATGC ACTTCTTCTCGCGTATTTGCACA
7010	Table 1	NA	469E12	-1	GGGGCTCAACCTGTGACTTACTGCT AACTAACATCAAAGGAAAGCTGG
7011	Table 1	NA	469F8	-1	ATGATCATTGATAGATATTCTAAGAG CATGCAGGAATGAGGATGCGTGCC
7012	Table 1	NA	469G8	-1	GACAACAAACCTGCTTGCTTGGTTAC CCACAGCGCACTGAGTATAGAAGT
7013	Table 1	NA	470B2	-1	TCITCAATTATTCTGCTCTAAGGCA GTGTCTGTCTTCCACCCTCCCGC
7014	Table 1	Hs.118174	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(2082,7460)	-1	TGAGTATTTTAAATCCCTGTTTGG ATGCTTCCAGCTAAATAGTCTACCT
7015	Table 1	NA	470C3	-1	TGGGTTTACTCAGATCTTCTCCTTCTT AAGTGAGAGTTTAACTACATTTT
7016	Table 1	NA	470D5	-1	GTCCAGAGCTAGAAGAACCAAGTCTT CCTTTCTTCATTCTGTTCAAGT
7017	Table 1	NA	470E1	-1	CTTCTCTTAGGATCTGGAGGGAGGG GAGTGTAGAGCTTGTGAGCCATG
7018	Table 1	NA	470E5	-1	CTGAACGAACCAAGTCTTTTGGACTA CCAGTTCTTGAAGTGAAGCTCAGA
7019	Table 1	NA	470F3	-1	AACAAAAGCACTGACAAGCTCATATG AACAGGCTAAAAAGTGAGTGAAGT
7020	Table 1	NA	470G6	-1	TTCTCTTTCTATCTAGCTAAATTGC CTGTGCGCCTCCCATCCTCTCA
7021	Table 1	NA	470B8	-1	ACACACTTGATAAATTGACCCGATGC AAACCGCAAGAATCCAAATCAGCT
7022	Table 1	NA	470G10	-1	ATAGTAGGTGAGCCAGTAGTGTGAAT GCTTGTCAAGCTTCCAAGGATGGA
7023	Table 1	NA	471D8	-1	AACCACCACCCAGCTTCTGTGTACAA GCAGGGACTCTGGCTACAGTGCTA
7024	Table 1	NA	471F1	-1	TTTCTCCCCCTCCCTCCCAATCCAC AAAACACGTAATTCTGACTATCCA
7025	Table 1	NA	471F4	-1	CAACATTCAAAAACTGGTCCCCGAA TTAGTGAGAAGGTTCCAGGAGTGC
7026	Table 1	NA	471F6	-1	GAGAGATTATAGCACAGTCTCCAGG GCTCAGTCAGGTCTCCGAGCAA
7027	Table 1	NA	471E9	-1	TTCAATGCTTTGTCTCCCTCGCAG ATGTTTAGAACAGATCTCTCTCT
7028	Table 1	NA	471E11	-1	TCCCTCTCTCAGGGCTGGGAAAGAAA GGTTCATCTTCACTCAGATGCAAG
7029	Table 1	NA	471H11	-1	TTCTGTTGGTCTGCCAGCTCATCCAT TCATCCATCACTGCCAGCTAGAC
7030	Table 1	NA	473E4	-1	ACACAGTTTTGGCTCCCTTATTTCC CCGTAAGTCAAAACATTTCCATGCA
7031	Table 1	NA	473F3	-1	ACCAAATCGAAAAATACAGAATGCC TGTAATTGAGTCACACCTTAAAA
7032	Table 1	NA	473E11	-1	GAGTCCATAAATCTGCATTTCATGTA GTTGTAAGACTTTCTCCCAAGGT
7033	Table 1	NA	476C1	-1	TCCATTGAGTTTTCTTCCCATCTCTC ACAGTTGATTGTTCTGTCCTTC

Table 8

7034	Table 1	NA	476D3	-1	AAAATTGAGCCCTCCTGGATTACAGT GCCCCAATGAAAGTCCCCAACTAG
7035	Table 1	NA	476F5	-1	TTTAACAGGAAAAAGCCCCAAATTATTT TTATGCTGTCTACAATCTGGGCC
7036	Table 1	NA	476G3	-1	AGTTGCACTGGTTGTTCTTGGCTGCG GTGCTTCTCACACAGAAGCCCCAG
7037	Table 2	NA	476G4	-1	TTTCCTTTTTCCCTTGTCCTTGCCCTT CCCCATCACCGAATCCCCCTTC
7038	Table 1	NA	476A10	-1	CTCCACGCGCTGGCCGTAGTCCAGA GCTTCTTCTTTTCATGGTTGGGTT
7039	Table 1	NA	476G8	-1	GCCAGTGTACGTTGCCAGGCATTTC TGTAAGAGAAAACTCAATAGCCA
7040	Table 1	NA	476H10	-1	CCGTCTTCTTTTGGGTGTTTCTCCT AGTTTCGGCGGAAATCAGAGTTCA
7041	Table 2	NA	477E1	-1	ATGAACCTCACCTGCTCTGCAGTGC AGTTTTGATTTTAGTCCCAGCAAA
7042	Table 1	NA	477E6	-1	AGATATAGATGGTAAATGTGATGCA ATGTAAAAAATGGTAATACACACAC TCTCCA
7043	Table 2	NA	477A11	-1	TGAGTGGGCTTCTCTTATGGTACAGT CTCTTCTCTATGAGGGGCTTCAAA
7044	Table 1	NA	477D9	-1	TGGGCTTCCAAATGGTACAATGGAGT AATCAAGCTCATGGACTGAGAGTT
7045	Table 1	NA	477D10	-1	CTTGAAGCTACTTGTCCCTTTCTGTG CCAGACCACCTAATGGCTACCCAC
7046	Table 2	NA	480A3	-1	TTCCCAGGGCGCTCCATCTACAGCCT TACTGTGACTCCACTCAGCACCAG
7047	Table 1	NA	480B5	-1	ATTCCCCCTAAGCTCCTGTCCCCCGC CATGCACGACTGGTCACATCAAAA
7048	Table 1	NA	480D2	-1	AAGACACACCCCTCCTGTTTAATAAA AGTTGTCCCTCGACATGCATAAT
7049	Table 1	NA	480E2	-1	CCTGGTTACAATAATGAACTGTCTGT GGAGTAAAGAGGGAAACATGACCA
7050	Table 1	NA	480E3	-1	AGAACCCACACACTGGGAGACAATAA CTGCCATTATATAACCAACAGAA
7051	Table 1	NA	480F3	-1	CGCCACTGCTTAAAGATTACAGACAA TTCCCAGGTAAAGTTGCCAGGACT
7052	Table 1	NA	480G4	-1	ACAATGATGTTTGAACGCACTCTGA ATCTGTGAAAGCTAGATAAGTCCT
7053	Table 1	NA	480C8	-1	GCCTTCTCTCTCTCCCTCTTGGGCC TATGTCTAGATAAGCCTGTTAAA
7054	Table 1	NA	480D9	-1	TGTCAAGATGACAGATCTTAATCCAG AGTGGAGGCTCGTTCGGCCTGGAG
7055	Table 1	NA	480E7	-1	TTTATGTTTCAGCCTCTTCTCTCCCG TTGAGTCTGCCACAAGTCCTGC
7056	Table 1	NA	480E11	-1	ATTGTCCAGGTGACTTGACACTTGCC TACCGGAAAAAGTTGGGATGTTCTT
7057	Table 1	NA	480F8	-1	TAAATATGCCCTAATTTAAAGGGCG CAGGGTCCCACAACAAGCCACAGA
7058	Table 1	NA	487F11	-1	AAATCTCTTCTCAGCTTCTGTTTGCA TTTAATCACCAGGTTTTAGCGC
7059	Table 3A	NA	499G1	-1	GCTACTGATGGGTGGCCCTTTATTCT TGTCTTTATTTGTTGTGTCAGGA
7060	Table 1	NA	518F10	-1	AAAAATTGGTAGCTGCCCCCATGTGG TATGATGTTAATTTGAACAACAT
7061	Table 3A	NA	524A12	-1	ACCCGGCAGCTCTCCTCAACCCCTTA ATTCTTTTCCAGCTTTTCATATTA
7062	Table 1	NA	526B9	-1	CTCAAGAGGGCATAGACATCCACAC GAGGACTGCATTGTCAGGGTAAC
7063	Table 1	NA	583B5	-1	AACAAATACCCAATTAAGTGTATTCCC CTTTCCCTATGACTGCTGGTGT
7064	Table 1	NA	583D6	-1	CCGTTGTCGGAAGCTTGCTTCCAAC TAAAGACCAGAGATGGGAGGGAGT
7065	Table 1	NA	583G8	-1	TTTAGCCCAAAGAAGACTTTCGCATA AATTCTGCCGTAACCTTGTTGGA
7066	Table 3A	NA	584A1	-1	CAAAGCAGCAAATACAGACACACAA CAATCCTTGGCCTGAGCAGAACAA
7067	Table 1	NA	584D3	-1	ATATGAAGATGGATTGGATGAGGACT GACAAAACGAAGACATGCCGGGCC
7068	Table 3A	NA	DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12 Contains t	-1	ATGCCTAGTCAGTCAGTATTCTTCTT GCTGCAGGTGTCATAAAACCCAC
7069	Table 3A	NA	591H9	-1	CCTTCGCATTCCCCATCCATGCTCC AAGATAATAGATTTTTCTTTAAAA

Table 8

7070	Table 3A	Hs.6179	DNA sequence from clone RP3-434P1 on chromosome 22. Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDELR (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3, the DDX17 gene for DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD), ESTs, STSs, GSSs and six putative CpG islands /cds=(307,2259) 602388170F1 cDNA, 5' end /clone=IMAGE:4517129 /clone_end=5'	-1	GGGGAACACTTTGGTTTGAAGCACAGACAGTTTGCCATGTTTCTTCTG
7071	Table 1	Hs.44577		-1	ACTGAATGGTCGAAATCACATATGCA CCACACATACTGATCTTAAGTAAC
7072	Table 3A	Hs.108124	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	-1	CGAGGTACAGCAAAGCGACCCTTGG TGTCATAGATCAGACGGAAATCTC
7073	Table 1	NA	119F12	-1	TACAGAAGAGCAGAGACCAACCTTCT CAAAGTTGGTGAGTATTAACCCAG
7074	Table 1	NA	119G10	-1	CCAGATTTGCTGATGTGTAGGTAGT TGTGGCACACTCACCTGTCTTTCC
7075	Table 1	NA	485A6	-1	CTTTCCAGGTTTTCCCTTTCCGCCAT TGTTTTCCGCTCGCTAAAGTGAC
7076	Table 1	NA	485D5	-1	TTGAACATTGCGAAAGTAACATCTCT CACTCCCAACACCACAGCTTATCG
7077	Table 1	NA	489H9	-1	AGTAACCAACCAAGCATAGTTTTAGA AGGGCTTTGCGAAACCTAGCCTTT
7078	Table 2	NA	494B11	-1	TCCTTCCGCCCGGCGAGGTCAG TATCTTCCGCTGCTGCTTTTGTGTT
7079	Table 1	NA	478E5	-1	GCTCTGAAACCCCTGGAACCTTGAG CCTAAATGTATTTTACAATCTT
7080	Table 1	NA	478G6	-1	ATCTTTGATGTGAAGCCCTTAAAAAT AACGTGAAGGTGCCAGCTTGCA
7081	Table 3A	NA	478H3	-1	ACCCAGCCTGATGTTCATCTTTTCCC CCTCTTCATTTTCTTCTTTGTTT
7082	Table 1	NA	478C7	-1	AGAAAGACTAACACCAGAAATCATGC TGCAACACCAGAACATCCTTTGGA
7083	Table 1	NA	478G8	-1	TCACAAAATATGGCTCAAGGAGTATA AATCCCTCTCACGCACCCACAAA
7084	Table 1	NA	478H7	-1	ACTAACCAACCAATGAGAATACTACT TACCTCCACCCATGCTGTGAACCC
7085	Table 3A	NA	479B4	-1	TGACCGCCTCAAAGACCAAAAGGACT CTACTCCATATTTCTCACTGTCT
7086	Table 1	NA	479D2	-1	GAATGACCACCTGACGATTCAGAGC TCACCTTCTTGTCTTCTCAGCTGTT
7087	Table 1	NA	479G2	-1	TTGGTAGAAACCAACCAACCAATAAAA TTCCAAGCCTGTACTGGTCAGCC
7088	Table 1	NA	479G3	-1	CATAAGTTGGGTGAAGAAATGGTGGT TTTAATCAGTAATATAGTCCCCC
7089	Table 1	NA	479G5	-1	TTCTCATCTCAATATCCCCCAGAGCC CCAGTACCTCATAATACAAGACTT
7090	Table 1	NA	479G6	-1	CTATCAGGCCCTCCAGATAGTCTTCT ATAAACCAATGATTGACGAGACT
7091	Table 1	NA	479H4	-1	TACCCAAAGTCTATTGTAAGTGCAT CTTTTCTATTAGACTGGAAGCTCC
7092	Table 1	NA	479H5	-1	GATGGTTGAGCAACTGAGGAGCTCA GGGTGACGGGTCCACAGAGCACAGA
7093	Table 1	NA	479H6	-1	AGAAATTAGAAGATGACTACCATTTG CTAAAGTCTATCCACATGCCAGCA
7094	Table 1	NA	479G12	-1	CCCCCTCGACCCCTCACACCCCTTTC CAGAGAGGCCCTTAAGATTCCCAT
7095	Table 1	NA	479H12	-1	TGTAAGGTTTCATAAATTTAGAGACC CTAGCCAGTCAGTGACAATATGCA
7096	Table 1	NA	482A5	-1	GAGTTGCTTATTCCAGTCTCTCTAAG ATATATCTCCCTTTTAGTTGCTGAC
7097	Table 3A	NA	483G5	-1	TGGTGTAAATGAACATGCCGATTGCC TTTATGGCCAGTTTGAGTCCTTCC
7098	Table 1	NA	486C4	-1	AGGGAACCCCAAAGAGTTAAACCAAG GACCACTATTTGATAGTCAACAAA
7099	Table 1	NA	490F10	-1	GTGGTAAATGAGAGCATTACAGACCA CCCACATCAGCCTAAATATAATT
7100	Table 1	NA	493C2	-1	CCACCAACCCCAACAGGCCGGGACA AATGCAATACCATACAGAAACACAG
7101	Table 1	NA	58G4	-1	GGCCAAACTTCTTACTCTGCCATTT GTTCAATGTCCTAATGAGCATGAA
7102	Table 3A	Hs.169370	DNA sequence from PAC 86H14 on chromosome 6q21-22. Contains FYN (P59-FYN, SYN, SLK) gene coding for two isoforms. Contains ESTs and STSs /cds=(12,1708)	-1	ATCAATCGGGCCAATCCGAAGTCAGC AATCTTGATATGAGTCCATTCCC

Table 8

7103	Table 1	NA			598H2	-1	TATTTTTAACAAAATCACACGGAAGG ATTTTCCTTCCCGTCCCATGTGTTG
7104	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	-1	CAGATAGTGGTATTGGGTGCTGGG CTTGCTGACCTGAGGAGGTGGCTG
7105	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element, mRNA	-1	AACCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAATAGGGAAGCC
7106	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	-1	GCATTTAGGAAAGACAGGTGAGTGTG CCACAACCTACCTAACACATCAGCA
7107	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element; contains	-1	TTACTTTGTCTTCTCTCACCATCCTAA AACGTTGTTTTGCTGAGCATGAA
7108	Table 3A	NA	AF249845	8099620	Isolate Siddi 10 hypervariable region I, mitochondrial sequence	-1	CCCCAGACGAAAAATACCAATGCATG GAGAGCTCCCGTGAGTGGTTAATA
7109	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	-1	GCCTAAGTTTCCAGAAGACTTTGACG ATGGAGAGCATGCAAAGCAGGTAA
7110	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	-1	TTTTGCAGTTCAAGGATTGGTGGGAA ACGTTTGATGTGTTGGGGTGGGG
7111	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element, mRNA s	-1	AATAGATTTCATTTCTTCTTCGAGT TAGTTGGGTATTGGGACCTTGAA
7112	Table 3A	NA	AW379049	6883708	RC3-HT0230-201199-013-c12 HT0230 cDNA, mRNA sequence	-1	CGACGGTGTCTGGAGTTTCGATGAG ACATGTAAGTAAGAGTTCTGTGCA
7113	Table 3A	Hs.232000	AW380881	6885540	UI-H-B10p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	ATATTCCAGCATGGCTGTGAAATGG ATTTGAATTACCGGATACATGCA
7114	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1	ACTGGTTTTCTATTCTAGTGTCCCCCA CCCGTCTAGTTTCATTTCTCTGA
7115	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1	TTGGGAGTCACCAGGTTAAAGCAAAG CCTCAGTCACTGAAAGCAGAACT
7116	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1	TCCTGTGCTCCAGAATTAGTGATTGC TTTGGTGCCTTAACCTGAAGTGGGA
7117	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1	CATCTGCTCTGCTTCTCCACACACTA GAAACACCACTGCCCCATCCATG
7118	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1	TCTGTGATTTATAGACTGTTTTCAGGA AACGATCTTCCCATCTGTGGTGA
7119	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1	TCATTTCAGGTCTAATAAACCACTAA CCTCGGCAGCACTGGAGCGTCTG
7120	Table 3A	NA	AW858490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1	AGCTTAGGATATCTATTAGTGTCACT GTTCCGGGCAAGAGGCCTAAAGGG
7121	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1	TGGGAACACACTGGCCCATTTATATAG AGAAAAATAAACATGATCCCCAT
7122	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	-1	TTGCTTGATTTCCCAACCACTACCT GAAGGTGGCTTATGGTCTACAGCT
7123	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1	TTCCACCACCTCAAGACTGGGGGCA GGTAGAGAAGACAAGCATAAGTACA
7124	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1	TTCTTCTGCTGCCCTAACAGAAATGTT CTTCTCTTGCTTCCACACCCCTCC
7125	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1	CAGCACATCTTCTGGTTTACAAGTTG GGTAACATGAAAGCTGGAGATGC
7126	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1	TATCTAAATCTACCTTTAGCATCCAA CTAGCTACCGTCTGGCACTGGCC
7127	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1	TCCAATGCTCAAGTCACTCTGAGTCT TTGCTGGTGTCAACCTACAATGCC
7128	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	-1	ACCTCACTATAGTAGCCATTAGGTAA AGATGGGCCATATCCAATGGGCT
7129	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1	AAGAACTATTCTTTGAGAATCTTTCC TACTGGGAGTTACTGCTGTGATT
7130	Table 3A	NA	BE178880	8658032	PM1-HT0809-060300-001-g03 HT0809 cDNA, mRNA sequence	-1	TCTGTGTGAACATACATACAGACTT TGATTCTACCTGTGCTGACCACTT
7131	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor- HGSC project=TCBA cDNA clone T mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1	GTGGAGCTGTGTGGCCTTGTGGATG CGGGCACTCTCTACACCTTCAGGTA
7132	Table 3A	Hs.11050	BE763412	10193336	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	-1	TGTCAGTGGCTCTCACTTTGTTTGA ATTGTTGCTTTGGGAAAAACAG
7133	Table 3A	NA	BF330908	11301656	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1	GATGCAGTGGGTTAGGGGTTGGGGG TACAGACTGACTTGAGCTCGGAGTC
7134	Table 3A	NA	BF357523	11316597	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	-1	TCAGGCACCTCAGTAAAGGCAAGACTT GAGTGATACATAAAGTCAGTTACA
7135	Table 3A	NA	BF364413	11326438		-1	CCTTGGGCTGAGTTTGCTGGTCTGTA AGATTACAGTTTGGTTAGAGAGA

Table 8

7136	Table 3A	NA	BF373638	11335683	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAAACAAAGTGTTCGAATCCTC TATTAAACCCATTAAACCAAGAGTT
7137	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCATTACACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
7138	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAGTGTGATTAGAGCAGCTGGAAGT AGCAGAGGAGGTGGAAGTTAGTCC
7139	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAACAGAGCTGGTTGTGT GATACCTATGCTGGGTGGAAGACT
7140	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGACTATCTTACCGGCTCCAGTA AACTCTGAACAATGTACCAGCTAA
7141	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTCAACAGAAATC ACCGACATGAGGAAGCATCACGCT
7142	Table 3A	NA	BF805164	12134153	QV1-CI0173-061100-456-f03 CI0173 cDNA, mRNA sequence	-1	AGGAACATGGCTGAGCATATAAAAA GAATTGAATTCCTACTTTTGTAAAC CTG
7143	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	-1	GGTGCTGCCATAGGTGCCAGTAATG ACCGTTTATGCGGAAATCAATTACA
7144	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAGGTGGATCAC
7145	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCTTTGATCTTCTG AGAATTAATAGAGATTTTCATGGCA
7146	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	-1	CCAAAAGGAGAAAGATGACTAGGGT CACACTTGAGGATTTGCCAGGTGGG
7147	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	-1	GCATCTCTTTGAAGACGGGAAGTGT ACTTCAGGTTCTTTCTGTTTACG
7148	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	-1	GGCTCATTTTGGTTTTAAAGTCTTCT ATGCCATCCAGGGGAGGAGGAT
7149	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	-1	GACTGTGGACACCTCTCACTGTGTCT TCTTGGCAGGCAGAGCTTACTGAC
7150	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	-1	GCAGGGTGCAGAGCTTCACAGCAGG TAGGAAGAAGTAACTAAGTGGAAAC
7151	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	-1	CAGCTAAAGCCGTAGGTCAATTGTGAC TGTCCCTGGGATGTGGATTACTCT
7152	Table 3A	NA	BF904425	12295884	CM1-MT0245-211200-662-d02 MT0245 cDNA, mRNA sequence	-1	CCAGAATGCAGCCTACACAGCAAAATA TCAATGGACTTGGGTAGCCCTGC
7153	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	TTTAAACCAAGGTCTGGAAAAGGAAG GAGAGGAGGGCATTTTAGAGAAGA
7154	Table 3A	NA	BF926187	12323197	CM2-NT0193-301100-562-c07 NT0193 cDNA, mRNA sequence	-1	GTGGCTTCGTAATAAGAGAGCAGT CACTGTGGAACCTACCAATGGCGA
7155	Table 3A	NA	BF928644	12326772	QV3-NT0216-081200-517-g03 NT0216 cDNA, mRNA sequence	-1	CACACCACAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
7156	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TGGAGAAAATGAGAGACAGACAGTG AGTGAGAAAGTCAGCGAAAAGGAAA
7157	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	ACCTACTGTGTAGATTATCCCTGT CTCCACACTGCCAGAACTTACCA
7158	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 89881 cDNA clone xs425, mRNA sequence	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAAGCACCACTATGG
7159	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f48, mRNA sequence	-1	TCCCAGAGCAACAACCTAAGTCTCAAC TAATGGACACCAACACCCCACTGA
7160	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	CCACAGAATGGGCATGTAGTATTGAG ATTTGAATCATCTGCTGCCAGCC
7161	db mining	Hs.661	NM_004146	10764846	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18) (NDUF7), mRNA /cds=(22,435)	1	ACCTCATCCGGCTGCTCAAGTGCAAG CGTGACAGCTTCCCCAATTCCTG
7162	db mining	Hs.943	NM_004221	4758811	natural killer cell transcript 4 (NK4), mRNA /cds=(59,763)	1	GACCTGGTGTGTCGCCCTGGCATC TTAATAAAACCTGCTTATACCTCCC
7163	db mining	Hs.1063	NM_003093	4507126	small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA /cds=(15,494)	1	GCATAAGGAAGACTTGCTCCCTGTCT CTATGAAAGAGAATAGTTTTGGAG
7164	db mining	Hs.1321	NM_000505	9961354	coagulation factor XII (Hageman factor) (F12), mRNA /cds=(49,1898)	1	GGGACTCATCTTTCCTCCTTGGTGA TTCCGCAGTGAGAGAGTGCTGGG
7165	db mining	Hs.288858	NM_003903	14110370	prefoldin 5 (PFDN5), mRNA /cds=(423,928)	1	AGACTGGATCGCACACCTTTGCAACA GATGTGTTCTGATTCTCTGAACCT
7166	db mining	Hs.1975	NM_030794	13540575	hypothetical protein FLJ21007 (FLJ21007), mRNA /cds=(257,2212)	1	AAGCAAATACCTTTTACAAGTGAAAG GAAGAATTTTCTTCTGCCGTC
7167	db mining	Hs.3804	NM_014045	13027587	DKFZP564C1940 protein (DKFZP564C1940), mRNA /cds=(565,1260)	1	GCAACAAATGCTTCTATTCATAGCT ACGGCATTGCTCAGTAAGTTGAGG
7168	db mining	Hs.3832	NM_032493	14210503	clathrin-associated protein AP47 (AP47), mRNA /cds=(76,1347)	1	TCCGTGTAGAGGTTACAGCCTTTTAT GCTGTTGAGCTCCAGGTACCAAA
7169	db mining	Hs.4113	NM_006821	5729723	S-adenosylhomocysteine hydrolase-like 1 (AHCYL1), mRNA /cds=(47,1549)	1	GCCCCTTGGATTTATAGTATAGCCC TTCCTCGACTCCACCAAGCTTGC
7170	db mining	Hs.83848	NM_000991	13904865	triosephosphate isomerase 1 (TPI1), mRNA /cds=(34,783)	1	AAGAGCTCCTGAGCCCCCTGCCCCC AGAGCAATAAAGTCAGCTGGCTTTC
7171	db mining	Hs.5076	AK025781	10438401	cDNA: FLJ22128 fis, clone HEP19543 /cds=UNKNOWN	1	GCTCAACATGGAAGAAGGTACAGAA AGTGATGTGTTCAAAACATTAGCA

Table 8

7172	db mining	Hs.5298	NM_015999	7705760	CGI-45 protein (LOC51094), mRNA /cds=(182,1294)	1	TTATATACCCTGGTCCCCTCTTTCTAG GGCCTGGATCTGCTTATAGAGCA GTTTACTCCGTCCTATCACTGGTGT GGCTGTGGGCAACCACTTATTGC
7173	db mining	Hs.5473	AW953785	8143468	602659796F1 cDNA, 5' end /clone=IMAGE:4802950 /clone_end=5'	1	
7174	db mining	Hs.5831	NM_003254	4507508	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA /cds=(62,685)	1	GAACTGAAGCCTGCACAGTGTCCAC CCTGTTCCCACTCCCCTCTTTCTTC
7175	db mining	Hs.5890	BF698885	11984293	hypothetical protein FLJ23306 (FLJ23306), mRNA /cds=(562,930)	1	GAAGACCAAGAGAGACAACAGACGC AGCAAACAGCCGAAGCACCAGACAA
7176	db mining	Hs.6211	NM_015846	7710138	methy-CpG binding domain protein 1 (MBD1), transcript variant 1, mRNA /cds=(139,1956)	1	AATTCAGAAAATTGTTGGGAGGACAG CCCCTTTGTGAACCTTGTTGGGG
7177	db mining	Hs.6285	AL080220	5262711	mRNA; cDNA DKFZp586P0123 (from clone DKFZp586P0123); partial cds /cds=(0,1067)	1	TTTACCCAGCTCTGAAGGTCATTGTT CTTGCTGTGTTTGAATAAAATCA
7178	db mining	Hs.6441	AL110197	5817115	mRNA; cDNA DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN	1	GTCTCTGATGCTTTGTATCATTCTGA GCAATCGCTCGGTCCGTGGACAA
7179	db mining	Hs.6459	NM_024531	13375681	hypothetical protein FLJ11856 (FLJ11856), mRNA /cds=(239,1576)	1	GGTAAGCCCCGTGAGCCTGGGACCTA CATGTGGTTTGGCTAATAAACATT
7180	db mining	Hs.6616	AL524742	12768235	AL524742 cDNA /clone=CS0DC008Y107-(5-prime)	1	TCTGGCTCTGACCGGTTGATGGCCTT GAGCGAATGAATCATGAAATTGA
7181	db mining	Hs.6650	NM_007259	6005775	vacuolar protein sorting 45B (yeast homolog) (VPS45B), mRNA /cds=(33,1745)	1	TGCCCTACATAGCAATTTCTGTGGC ACTGAGAAACCATGTATGACCACA
7182	db mining	Hs.6763	NM_015310	7662395	KIAA0942 protein (KIAA0942), mRNA /cds=(52,1656)	1	GCAGTGTACTGTGTGCAATACCAAGG GCATAGCTCCCTGTAATTGGGAA
7183	db mining	Hs.6780	NM_007284	6005845	protein tyrosine kinase 9-like (A8-related protein) (PTK9L), mRNA /cds=(104,1153)	1	CTGAGACTAGGGTCCCAGCACAGCC CAGAAACCTTTGGCCACAAGAAGTG
7184	db mining	Hs.6817	NM_025200	13376793	putative oncogene protein hlc14-06-p (HLC14-06-P), mRNA /cds=(51,635)	1	TGCGCTTCCATGGTTTAAATGCAG TAAATAACATTTCTGGATGAGACT
7185	db mining	Hs.7709	U79457	4205083	Homo sapiens, Similar to VWW domain binding protein 1, clone MGC:15305 IMAGE:4309279, mRNA, complete cds /cds=(162,971)	1	GCTTTACCCCGCAGGACATACACAG GAGCCTTTGATCTCATTAAAGAGA
7186	db mining	Hs.7740	AF288741	14209837	oxysterol binding protein 2 (OSBP2), mRNA, complete cds /cds=(112,2748)	1	GGAATGTACTCTCCCCAACACTGTT TTGTTAGCGAGCACCTTTTGACCA
7187	db mining	Hs.8108	NM_021080	10835268	disabled (Drosophila) homolog 1 (DAB1), mRNA /cds=(765,2426)	1	ACTCGCTCAGAAGAGGGAACCTAAGC ATTTTGGCAACCAATGGGCAGATA
7188	db mining	Hs.8109	NM_022743	12232400	hypothetical protein FLJ21080 (FLJ21080), mRNA /cds=(127,1236)	1	AGCTGTGTGAACCTCTCTTATTGGAA ATTCTGTTCCGTGTTTGTGTAGGT
7189	db mining	Hs.8207	NM_020198	8910241	GK001 protein (GK001), mRNA /cds=(184,1635)	1	AGTCCCATACATTTGGACCATGGCAG CTAATTTTGTAACTTAAGCAITTC
7190	db mining	Hs.226627	BC007375	13938462	leptin receptor short form (db) mRNA, complete cds /cds=(0,2690)	1	CTGCCCCCTTCTGGACTTCGTGCCT TACTGAGTCTCTAAGACTTTTCT
7191	db mining	Hs.8768	NM_018243	8922711	hypothetical protein FLJ10849 (FLJ10849), mRNA /cds=(93,1382)	1	GGATAACATTTCTCATGAACCCACTG CCCCTCTGCATTTTCTCACTGGT
7192	db mining	Hs.8834	NM_006315	5454011	ring finger protein 3 (RNF3), mRNA /cds=(114,857)	1	CGCTTAAGAACATTGCCTCTGGGTGT CATGTGGACCACTCTGTAATAG
7193	db mining	Hs.9683	NM_006260	5453979	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor (PRKRI), mRNA /cds=(690,2204)	1	GGGTTCAATCCCTTCAGCTCAGGCG GACCATTAGATTTAAATCCACTT
7194	db mining	Hs.9825	NM_016062	7706342	CGI-128 protein (LOC51647), mRNA /cds=(35,526)	1	GCTCCTGCCAGGGCTGTTACCGTTGT TTTCTTGAATCACTCACAATGAGA
7195	db mining	Hs.10590	AL031685	9368423	DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18,CYK18)) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0757) and the 3' end of the gene for KIAA0939 (novel Sodium/hydrogen exchanger family member). Contains ESTs, STSs, GSSs and four putative CpG islands /cds=(2,688)	1	AATCTGGCGAAACCTTCGTTTGAGGG ACTGATGTGAGTGTATGTCCACCT
7196	db mining	Hs.11465	NM_004832	4758483	glutathione-S-transferase like; glutathione transferase omega (GSTT1p28), mRNA /cds=(8,734)	1	GACTATGGGCTCTGAAGGGGGCAGG AGTCAGCAATAAAGCTATGTCGTAT
7197	db mining	Hs.11538	NM_005720	5031600	actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1188)	1	AGGGAGGGGACAGATGGGGAGCTTT TCTTACCTATTCAAGGAATACGTGC

Table 8

7198	db mining	Hs.12707	AK023168	10434970	cDNA FLJ13106 fis, clone NT2RP3002455, highly similar to mRNA for KIAA0678 protein /cds=UNKNOWN	1	ACCTTCTGAAAGCTCAGAGTACACAT TAGTATGTATAACTGGCTTTACCA
7199	db mining	Hs.12785	AL031685	9368423	DNA sequence from clone RP5-963K23 on chromosome 20q13.11-13.2 Contains a KRT18 (Keratin type I, Cytoskeletal 18 (Cytokeratin 18, CK18, CYK18)) pseudogene, a gene for a novel protein, the gene for spermatogenesis associated protein PD1 (KIAA0757) and the 3' end of the gene for KIAA0939 (novel Sodium/hydrogen exchanger family member). Contains ESTs, STSs, GSSs and four putative CpG islands /cds=(0,1313)	1	TTTAAGGGAGTCAGGAATAGATGTAT GAACAGTCGTGTCACTGGATGCCT
7200	db mining	Hs.13323	NM_022752	12232416	hypothetical protein FLJ22059 (FLJ22059), mRNA /cds=(783,1967)	1	CCCACCTTCCACCTCTTAGCACTGGT GACCCCAAAATGAAACCATCAAT
7201	db mining	Hs.13659	AL080209	5262698	Hypothetical protein DKFZp586F2423	1	AGACCAGCAGTGTTTAAATCTAAATA CGTTGTGAGTCTGTTATCTGCTCT
7202	db mining	Hs.14089	NM_013379	7019510	dipeptidyl peptidase 7 (DPP7), mRNA /cds=(0,1478)	1	ACCTCGACCTCAGAGCCTCCACCCC AGAAGATCCTGCTCCGTGGTTGAG
7203	db mining	Hs.16488	NM_004343	5921996	calreticulin (CALR), mRNA /cds=(68,1321)	1	GGGCAGTGGGTCCAGATGGCTCA CACTGAGAATGTAAGAACTACAAAC
7204	db mining	Hs.16580	NM_018303	8922829	hypothetical protein FLJ11028 (FLJ11028), mRNA /cds=(31,2355)	1	TGGCCTTAAGTTTCTAATTCAAGCG GGTTTTGGAAAAATTTATGGTCT
7205	db mining	Hs.109438	AB028950	5689390	clone 24775 mRNA sequence /cds=UNKNOWN	1	TGCAGAGTTATAAGCCCCAACAGGT CATGCTCCAATAAAAAATGATTCTA
7206	db mining	Hs.18586	NM_014826	7662135	KIAA0451 gene product (KIAA0451), mRNA /cds=(1482,2219)	1	CCAAACAATGATGTGGATTCTTTTGC ACAGAAATATTTAAGGTGGGATGG
7207	db mining	Hs.19575	NM_015941	7706261	CGI-11 protein (LOC51608), mRNA /cds=(233,1684)	1	ACAAAAGTCAACTGTGTCTCTTTTCA AACCAAATGGGAGAAATGTTGC
7208	db mining	Hs.20529	AK025464	10437985	cDNA: FLJ21811 fis, clone HEP01037 /cds=UNKNOWN	1	GCTGGGGACTCTAGCCTCTGTGTTCA TAAAGACATTAGAAGTGGATGGA
7209	db mining	Hs.20725	NM_020963	14211539	Mov10 (Moloney leukemia virus 10, mouse) homolog (MOV10), mRNA /cds=(70,3081)	1	GGAGAATGACACATCAAGCTGCTAAC AATTGGGGGAAGGGGAAGGAAGAA
7210	db mining	Hs.343590	AB011104	3043587	601471579F1 cDNA, 5' end /clone=IMAGE:3874747 /clone_end=5'	1	ACCTGGGTTTAATACAGCTCACATCA CTGAATGTACACATGAGTTTAA
7211	db mining	Hs.23449	NM_018842	10047119	insulin receptor tyrosine kinase substrate (LOC55971), mRNA /cds=(333,1553)	1	CTTAAGGACGCCTTTGCGTGGCCCTT TATTACAGCCCAACACGGTAGGC
7212	db mining	Hs.23990	NM_017838	8923443	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) (NOLA2), mRNA /cds=(86,547)	1	TCCATCAGTGCCATTTCTGTAGAAC TAAAGGCTGTTCCAAGATGTGGG
7213	db mining	Hs.24024	NM_015376	7662333	KIAA0846 protein (KIAA0846), mRNA /cds=(272,2341)	1	ATCTGTAAAGCACTCAGAAGGCAGCC ATCCCTAGATGTGGTTTCATGTA
7214	db mining	Hs.334842	BC008330	14249901	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGGTTAGATTGTTTTCACTTGGTGAT CATGTCTTTTCCATGTGACCTGT
7215	db mining	Hs.24641	AK022982	10434687	cDNA FLJ12920 fis, clone NT2RP2004594 /cds=(96,2144)	1	CATGTCCCTTGAACATGATAGTTAC ATACACAGTTTCTCTCCACACAT
7216	db mining	Hs.321105	NM_015462	7661683	cDNA: FLJ21737 fis, clone COLF3396 /cds=UNKNOWN	1	AGGTTTTCATGTAACCTGTTCTAGGC TGTGGACATTGGTGTGGAGAGGTT
7217	db mining	Hs.26802	NM_021158	11056039	protein kinase domains containing protein similar to phosphoprotein C8FW (LOC57761), mRNA /cds=(294,1370)	1	GACACTTGGGGTCCACAATCCCAGG TCCATACTCTAGGTTTTGGATACCA
7218	db mining	Hs.26892	NM_018456	8922098	uncharacterized bone marrow protein BM040 (BM040), mRNA /cds=(357,749)	1	AGAAATGATTTCAGCTGAGTGAATC AGGAAGTGACAGTGATGACTGAAG
7219	db mining	Hs.27076	NM_003729	4506588	RNA 3'-terminal phosphate cyclase (RPC), mRNA /cds=(170,1270)	1	TCCTGAGAGATGGACAATGAAATATC AGTTGGTGGATATGTGTGATAGCT
7220	db mining	Hs.27445	NM_016209	7706428	unknown (LOC51693), mRNA /cds=(58,480)	1	CTTTCAGGGCAGGCAGCTGTGCATG TTCTCTCACTAAAGGCTCTGTGAG
7221	db mining	Hs.27633	NM_015456	7661663	DKFZP586B0519 protein (DKFZP586B0519), mRNA /cds=(75,1189)	1	GCTGGACACACGGTGAGATTTTCTCG TATGTAAATAAAGGCAATTTGGT
7222	db mining	Hs.28310	BG260891	12770707	602372491F1 cDNA, 5' end /clone=IMAGE:4480510 /clone_end=5'	1	CTCAACGAAAGGCTCACACTAACAGG GGAGGATTACAGCACCAACTACT
7223	db mining	Hs.28914	NM_000485	4502170	adenine phosphoribosyltransferase (APRT), mRNA /cds=(71,613)	1	CCACACTGAACCCAATTACACACAGC GGGAGAACGCAGTAAACAGCTTTC
7224	db mining	Hs.29893	AL133426	6562628	mRNA full length insert cDNA clone EUROMAGE 146397 /cds=UNKNOWN	1	AGGCCCTGGAAAAATTTTGTGCTTCCA ACGTGGCCTTCAATTCTTGCTTTT
7225	db mining	Hs.30120	BF970066	12337281	602272333F1 cDNA, 5' end /clone=IMAGE:4360233 /clone_end=5'	1	TATTAAGCTTGCCAGGCTCCTGTTC ATGAAGGTTCCCCACGGGTGGCC

Table 8

7226	db mining	Hs.30250	AF055376	3335147	short form transcription factor C-MAF (c-maf) mRNA, complete cds /cds=(807,1928)	1	GCTATACCACTGACTGTATTGAAAAC CAAAGTATTAGAGGGGAAACGCC
7227	db mining	Hs.30443	AL136599	13276698	mRNA; cDNA DKFZp584G1816 (from clone DKFZp564G1816); complete cds /cds=(137,3091)	1	TCGGGGTCAGTTAAGCCTCAGTATTC TTAGCTTTTGTGATTTTGCCACT
7228	db mining	Hs.31137	NM_006504	5729992	protein tyrosine phosphatase, receptor type, E (PTPRE), mRNA /cds=(51,2153)	1	ATGGTGCAAAACCTGGAACAGTATGA ATTCTGCTACAAAGTGGTACAAGA
7229	db mining	Hs.34114	NM_000702	4502270	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA /cds=(104,3166)	1	AGAAGCAGCGAGTGCATGGGCTAAT TATCATCAATCTTTATGTATTTGTT
7230	db mining	Hs.35254	NM_020119	9910221	hypothetical protein FLB6421 (FLB6421), mRNA /cds=(310,792)	1	GGAATGTTGCTGTGGGGGATTTCATT GTAACCTCCTTGTGAACGTCTCA
7231	db mining	Hs.38735	BG149337	12661367	nad26g06.x1 cDNA, 3' end /clone=IMAGE:3366730 /clone_end=3'	1	ATGCCAAATTCCTGACACGTGGCGTT TGAATAACCATGGAACGTTTCCA
7232	db mining	Hs.41322	AI655467	4739446	tt13b01.x1 cDNA, 3' end /clone=IMAGE:2240617 /clone_end=3'	1	ACATTCTGACTCCATCTGCGGCCCTCA TTAAGGTGATAGAAACATACTAGG
7233	db mining	Hs.42346	AY013295	11693027	calcineurin-binding protein calsarcin-1 mRNA, complete cds /cds=(131,925)	1	ATGATAATGTTGGCATCTGTGATAAA CTATCAATGAGGCTCCCATCATGC
7234	db mining	Hs.42699	AW956580	8146278	EST388665 cDNA	1	AGAGTCACATGTAGAAAAGCCTCCAG TATTAAGCTCCTGAATTCATTCT
7235	db mining	Hs.44131	AB023191	4589591	mRNA for KIA0974 protein, partial cds /cds=(0,1697)	1	ATGGCAACAATGCTGACAGCAAGCA GTAGATCCTCTGATTCCAATTACCA
7236	db mining	Hs.44441	BE295812	9179366	601176827F1 cDNA, 5' end /clone=IMAGE:3532039 /clone_end=5'	1	GGGAACCTCATTAAATTAGACAAGAA CACCAAGGCTATGACCACAGCAGC
7237	db mining	Hs.46919	AY007155	9956067	clone CDABP0095 mRNA sequence /cds=UNKNOWN	1	GGCTCACCAGAGTACCCAGAAGAAT CAGTATGGAATTAGAGGACAGTGGC
7238	db mining	Hs.56009	NM_006187	5453823	2'-5'-oligoadenylate synthetase 3 (100 kD) (OAS3), mRNA /cds=(34,3297)	1	ATTCAGGCCCTCAGCTTTTGGCAAT GGCCACCTGGTGTGGCATATTG
7239	db mining	Hs.57843	V63785	1371386	zd30g09.s1 cDNA, 3' end /clone=IMAGE:342208 /clone_end=3'	1	GCATACATAAAGGCAAGAATGACAA AAGGCTTAATCCACCTAGAGACA
7240	db mining	Hs.58373	BF339748	11286202	602034942F1 cDNA, 5' end /clone=IMAGE:4182851 /clone_end=5'	1	ATATAGTGGGAGACAAACACAGGAG GCGGGGGATATCATGTAGCAGAGC
7241	db mining	Hs.59236	NM_032139	14149802	hypothetical protein DKFZp434L0718 (DKFZp434L0718), mRNA /cds=(133,3285)	1	TCTAATGTGCCTTGGATATGTGCCAA ATGATGAAAAAGAACAGTAACT
7242	db mining	Hs.62408	NM_024660	13375912	hypothetical protein FLJ22573 (FLJ22573), mRNA /cds=(99,1166)	1	GCTTGGCTCATCTGGGGTTTGCTGG GCTTAACCCCAATAAAGAACTTTG
7243	db mining	Hs.63042	NM_018457	8922156	DKFZp564J157 protein (DKFZp564J157), mRNA /cds=(77,523)	1	CTCGGTTTGGAACTTACCTCTCC TCCTTAGCCCAATATGCTGTCTTG
7244	db mining	Hs.65648	NM_005105	4826971	RNA binding motif protein 8A (RBM8A), mRNA /cds=(12,536)	1	TCCAGGCCATTTTGCAGGGACTCTGA AGTGACCTTTAGTAGTAATAGTCT
7245	db mining	Hs.339868	NM_003974	4503358	oh47h10.s1 cDNA, 3' end /clone=IMAGE:1469827 /clone_end=3'	1	TGGCAGCCAGGAATGAGTATGACA ATGTTGTACTAAAGAAAGGCCCAAA
7246	db mining	Hs.75056	NM_003938	4501976	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA /cds=(209,3547)	1	AGAGAGAGACATATCACGCTGCTGTC ATGATTTTGTGTCAAGATGATCCA
7247	db mining	Hs.75082	NM_001665	4502218	ras homolog gene family, member G (rho G) (ARHG), mRNA /cds=(129,704)	1	CTTCTGGGACCTTTCTACCCCCAT CAGCATCAATAAAACCTCCTGTCT
7248	db mining	Hs.75309	NM_001961	4503482	eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(0,2576)	1	TAGATGATTTCTAGCAGGCAGGAAGT CCTGTGCGGTGTCAACATGAGCAC
7249	db mining	Hs.75725	NM_003564	4507356	transgelin 2 (TAGLN2), mRNA /cds=(73,672)	1	CCATGGTCTGGGGCTTGAGGAAGAT GAGTTTGTGATTAAATAAAGAT
7250	db mining	Hs.75770	NM_000321	4506434	retinoblastoma 1 (including osteosarcoma) (RB1), mRNA /cds=(138,2924)	1	AGGTCAAGGCTTACTATTCTGGGT CTTTTGCTACTAAGTTCACATTAG
7251	db mining	Hs.75790	NM_002642	4505794	phosphatidylinositol glycan, class C (PIGC), mRNA /cds=(293,1186)	1	TTTCTGGGACCTCTTGAATTACATG CTGTAACATATGAAGTGATGTGGT
7252	db mining	Hs.76057	NM_000403	9945333	galactose-4-epimerase, UDP- (GALE), mRNA /cds=(76,1122)	1	TGGCACAAACCTCCTCCCGAGGC ACTCATTATATTGCTCTGAAAGA
7253	db mining	Hs.76682	NM_032327	14150105	hypothetical protein MGC2993 (MGC2993), mRNA /cds=(158,1048)	1	TGAGGTCACTGCCACTTCTCATATGC TGCTTAAGGAGGACCAATAAAGG
7254	db mining	Hs.77268	NM_002826	13325074	quiescin Q6 (QSCN6), mRNA /cds=(75,2318)	1	CACGCTACCCCTGCCTTGGGAGGT GTGTGGAATAAATATTTTGTAA
7255	db mining	Hs.77290	NM_006755	5803186	transaldolase 1 (TALDO1), mRNA /cds=(50,1063)	1	AATGCAGAGATGGAAGTAGCGCAT CCTGAGGCTGGACTCCAGATCTG
7256	db mining	Hs.77805	NM_001696	4502316	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD (ATP6E), mRNA /cds=(75,755)	1	GTGGCACACCACTCCTCCAGCAGTA GTCGCTTACTGTTACCTGTTTAG
7257	db mining	Hs.78592	NM_001414	4503502	eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD) (EIF2B1), mRNA /cds=(10,927)	1	AGCAACAGTATTCTGCATGGTTCACT GCTTAAGAAAATGCCCTTCTGGAAT

Table 8

7258	db mining	Hs.78605	BC008159	13544048	Homo sapiens, clone IMAGE:3635549, mRNA, partial cds /cds=(0,891)	1	AAACATGTCCTGGAGAGTAGCCTGC TCCCACACTGTCACTGGATGTCAT
7259	db mining	Hs.78890	AF171938	5852969	NUMB isoform 1 (NUMB) mRNA, complete cds /cds=(270,2225)	1	CAGTTGCAGCCTCTTGACCTCGGATA ACAATAAGAGAGCTCATCTCATTT
7260	db mining	Hs.79150	NM_006430	5453604	chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(0,1619)	1	TGGGCTTGGCTTCCAGTTGGCATT GCCTGAAGTTGTATTGAAACAATT
7261	db mining	Hs.79259	NM_016404	7705476	hypothetical protein (HSPC152), mRNA /cds=(35,412)	1	TTCTGCCGTGTGTATCCCCAACCCCT GACCCAATGACACCAACACAGTG
7262	db mining	Hs.79356	NM_006762	5803055	Lysosomal-associated multispanning membrane protein-5 (LAPTM5), mRNA /cds=(75,863)	1	TGTGTGCGACAGGGAGGAAGTTTCA ATAAAGCAACAACAAGCTTCAAGGA
7263	db mining	Hs.79572	NM_001909	4503142	cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA /cds=(2,1240)	1	CTCCCCCTGGGGCGGTGAGAGCCCC AGCTGACATGGAAATACAGTTGTTG
7264	db mining	Hs.81337	NM_009587	6806889	lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant long, mRNA /cds=(56,1123)	1	CTCCACCACCTGACCAGAGTGTCTC TTCAGAGGACTGGCTCCTTTCCCA
7265	db mining	Hs.82030	NM_004184	7710155	tryptophanyl-tRNA synthetase (WARS), mRNA /cds=(187,1602)	1	CTCTGCCCTCCTGTCACCCACTAGAG TAAATAAACTTCCTTGGCTCCTAA
7266	db mining	Hs.82396	NM_016816	8051620	2',5'-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E18, mRNA /cds=(33,1235)	1	AAATTCAGCCTTGACTTCTTCTGT GCACCTGATGGGAGGTAATGTCT
7267	db mining	Hs.82933	BC008739	14250568	Homo sapiens, protein x 013, clone MGC:3073 IMAGE:3346340, mRNA, complete cds /cds=(101,325)	1	CTGTAGGCCAGGGTGAATGAAGTC AGCTCCTTTTATAGTTGAATACA
7268	db mining	Hs.83753	NM_003091	4507124	small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), mRNA /cds=(0,695)	1	TTGGCGGGCCATCCCAACAGGTGAT GACCCCAACAAGGAGGTAAGTGT
7269	db mining	Hs.85838	NM_004207	4759111	solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3), mRNA /cds=(62,1459)	1	GGAAGATGGAATAAACCTGCGTGTG GGTGGAGTGTCTCGTGCCGAATT
7270	db mining	Hs.306565	NM_013341	9558756	clone HQ0688 /cds=UNKNOWN	1	AGTGAGGACAATGTGGCTTGCTCCT TTTGAATCTACAGATAATGCATGT
7271	db mining	Hs.89497	NM_005573	5031876	lamin B1 (LMNB1), mRNA	1	GAGGGTGGGGAGGAGGTGGAGG GAGGGAAGGGTTTCTCTATTAATG
7272	db mining	Hs.89525	NM_004494	4758515	hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA /cds=(315,1037)	1	TGCTGACTGTAGCTTTGGAAGTTTAG CTCTGAGAACCGTAGATGATTCA
7273	db mining	Hs.92208	NM_003815	11497001	a disintegrin and metalloproteinase domain 15 (metargidin) (ADAM15), mRNA /cds=(7,2451)	1	GATTGAGGAAGGTCCGCACAGCCTG TCTCTGCTCAGTTGCAATAAACGTG
7274	db mining	Hs.103527	NM_003975	4503632	SH2 domain protein 2A (SH2D2A), mRNA /cds=(86,1255)	1	GATTCTTGCTGGCTAATAAATCATCA CCAACCTGCCTTCTCTACAGGGA
7275	db mining	Hs.104679	BF347362	11294957	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2208,2373)	1	AGATTCTTAGGGCAGCTTTGTTCCCC TTGGAGGGTTTTCCACACGGAGTC
7276	db mining	Hs.105749	AB011125	3043629	mRNA for KIAA0553 protein, partial cds /cds=(0,3289)	1	GCCATACTCTGGCTGCCTCTTTGCCCT TCCTAGGGGCACTTTCTTTAACTT
7277	db mining	Hs.105751	AL138761	8573811	DNA sequence from clone RP11-16H23 on chromosome 10. Contains the gene KIAA0204 (HSLK) for a protein kinase, the COL17A1 gene for collagen type XVII alpha 1 (BP180), ESTs and GSSs /cds=(0,3557)	1	TGCCTCTTATCTACTTGAGAGCAACA TGCTTTTCAATCATGGGATTGAC
7278	db mining	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	TGGACCTGTGACATTCTGGACTATTT CTGTGTTTATTTGTGGCCGAGTGT
7279	db mining	Hs.108371	NM_001950	12669914	E2F transcription factor 4, p107/p130-binding (E2F4), mRNA /cds=(62,1303)	1	TGAAGGTGTCTGTGACCTCTTTGATG TGCTGTCTCAACCTCTGACTGA
7280	db mining	Hs.109760	NM_002491	4505360	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3), mRNA /cds=(252,548)	1	CCTGGAGTCCCTGAATAAAGATAAGA AGCATCACTGAAGATAATACCTGG
7281	db mining	Hs.109857	AF151783	14248494	MEG3 (MEG3) mRNA, complete cds /cds=(52,2253)	1	TTGTCCCGAAGATTGCGCCTTTAGT GCCTTTTGAGGGGTTCCCATCATC
7282	db mining	Hs.306417	NM_014714	7662193	cDNA FLJ10935 fis, clone OVARC1000661 /cds=(250,936)	1	CTGCTAGGCTCTGCCACCGGCCAC CAACACTCCTGTGAATTCGAATAAAG
7283	db mining	Hs.114199	BG621594	13672965	602617003F1 cDNA, 5' end /clone=IMAGE:4730856 /clone_end=5'	1	TTAAATACTGTCAATTGGTTGGGAGG GGATTGCATTAATGATTAGTCCA
7284	db mining	Hs.118786	BF131637	10970677	601820457F1 cDNA, 5' end /clone=IMAGE:4052246 /clone_end=5'	1	CTCACACACGCAGGCACAGTCAGA ACAAACAGGAACAAAGCTACAACAC
7285	db mining	Hs.122559	NM_024872	13376307	hypothetical protein FLJ22570 (FLJ22570), mRNA /cds=(0,1490)	1	TGAATAGTGTGCAGACTCACAGATAA TAAAGCTCAGAGCAGCTCCCGGCA
7286	db mining	Hs.123373	AW983279	8153115	602853825F1 cDNA, 5' end /clone=IMAGE:4994982 /clone_end=5'	1	CCCACTGCTTACAGGAAGTTAAAGAA AGATCTGCTGGTAGTGTATTAGTCT

Table 8

7287	db mining	Hs.125078	AF090094	4063629	clone IMAGE 172979 /cds=UNKNOWN	1	CGAGCCGACCATGTCTTCATTTCGCTT CCACAAGAACC CGGAGGACAGAGC
7288	db mining	Hs.130740	AK000315	7020316	cDNA FLJ20308 fis, clone HEP07264 /cds=(90,126)	1	TTTTCCTCTTAGTCTCCTGGCTTTT TCCTTTCCCTTCCCTTCTCCACT
7289	db mining	Hs.132955	AL132665	6137021	mRNA; cDNA DKFZp566E034 (from clone DKFZp566E034); complete cds /cds=UNKNOWN	1	AACCCGTTGTGGAATTTATTGGAATT AACTGAGCCAAAGTGATTATGCAT
7290	db mining	Hs.133230	BC000085	12652672	Homo sapiens, ribosomal protein S15, clone MGC:2295 IMAGE:3507983, mRNA, complete cds /cds=(14,451)	1	GCCCCCGATCCTACACCTTGAGCCT CAGAGCACTGCTACTTTTTAAATA
7291	db mining	Hs.142677	AK024108	10436406	cDNA FLJ14046 fis, clone HEMBA1006461 /cds=UNKNOWN	1	AAGCGTCTCATGGAGTTCGGACTGGT TGGGGTGATAATATTGTTCTTT
7292	db mining	Hs.146170	NM_022842	12383093	hypothetical protein FLJ22869 (FLJ22869), mRNA /cds=(274,2223)	1	AAGCCAGGCTTTGGGATACAAGTTCT TTCCTCTTCATTGTATGCCGTGCA
7293	db mining	Hs.146550	Z82215	3135984	DNA sequence from clone RP1-6802 on chromosome 22 Contains the 5' end of the APOL2 gene for apolipoprotein L 2, the APOL gene for apolipoprotein L, the MYH9 gene for nonmuscle type myosin heavy chain 9. ESTs, STSs and GSSs /cds=(0,5882)	1	AGCTGTCAACACTACAGTAAGCTGGT TTACAGATGTTTCCACTGAGCAT
7294	db mining	Hs.149846	NM_002213	4504772	Integrin, beta 5 (ITGB5), mRNA /cds=(29,2419)	1	TGAAGGTACATCGTTTGCAAAATGTGA GTTTCCTCTCCTGTCCTGTTTGT
7295	db mining	Hs.151738	NM_004994	4826835	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (MMP9), mRNA /cds=(19,2142)	1	GGATACAACTGGTATTCTGTCTG AGGAAAGGAGGAGTGGAGGTGGG
7296	db mining	Hs.336451	NM_024519	13375657	Nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis- alpha)	1	CTGCCGCTGCCAGCCACATCCCTT GGTTTTGTATTTATTACAGAGTT
7297	db mining	Hs.154276	NM_001186	4502352	BTB and CNC homology 1, basic leucine zipper transcription factor 1 (BACH1), mRNA /cds=(118,2328)	1	TGCAGTAGACGATACAGGTTCATGT GGACACTCAGTCACATTAACAAC
7298	db mining	Hs.155975	NM_005608	5032004	protein tyrosine phosphatase, receptor type, C-associated protein (PTPRCAP), mRNA /cds=(63,683)	1	CCCCAACCCAGGCATCAGGCAACC ATTTGAAATAAACTCCTTCAGCCT
7299	db mining	Hs.159410	NM_014484	7657338	molybdopterin synthase sulfurylase (MOCS3), mRNA /cds=(2,1384)	1	GTAAGGAGGAGTGGTATAGTCTGA TGAGAAAGATGTGGATTGCCATAA
7300	db mining	Hs.160999	AV648418	9869432	cDNA FLJ13696 fis, clone /clone=GLCBJC04 /clone_end=3'	1	CACTTGTTCAATCATGGAACCTTCTA GAACGCTGCCACTCTTCAAAGGCT
7301	db mining	Hs.164036	NM_002076	4504060	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), mRNA /cds=(87,1745)	1	TCATCACAGTGTGTAAGTTGCAAA TTCAAAACATGTACCCCAAGCTCT
7302	db mining	Hs.164478	NM_022481	11968002	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 (FLJ21939), mRNA /cds=(379,1557)	1	ACAACCTGATCATTGAAGCCAACCTT GTCCAGCACATTCTTAAGTCTCT
7303	db mining	Hs.169615	NM_023080	12751496	hypothetical protein FLJ20989 (FLJ20989), mRNA /cds=(52,741)	1	ACTTGATTAGGCTCCGGTTTTCTTT GGCTTCTGCTTTTCACTGAATGGC
7304	db mining	Hs.171811	AK023758	10435787	cDNA FLJ13696 fis, clone PLACE2000140 /cds=UNKNOWN	1	TTGCAGACAAATTCCTCTGAGCTTAG CTAGGAGTTTCACTTCTCTCTGT
7305	db mining	Hs.171992	NM_002843	4506314	protein tyrosine phosphatase, receptor type, J (PTPRJ), mRNA /cds=(349,4362)	1	ACAGTAGCTTAGCATCAGAGGTTTGC TTCTCAGTAACATTTCTGTCTC
7306	db mining	Hs.173373	AB023148	4589505	mRNA for KIAA0931 protein, partial cds /cds=(0,2204)	1	ATGTGAGCCAGAGCATGTTGCAGCAA ATCTATTGTTTGTAAAAATAACAA
7307	db mining	Hs.173638	NM_030756	13540470	transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), mRNA /cds=(307,2097)	1	TTGTGCCATGTATCCAGGTTAGTTG ATGTTTATCGAGTTCACTTGGTCAA
7308	db mining	Hs.177534	NM_007207	13518225	dual specificity phosphatase 10 (DUSP10), mRNA /cds=(142,1590)	1	AGCCCAACCATTAATAATTAATACAA CTTGGTTTCTCCCCCTTTTCTCT
7309	db mining	Hs.177592	NM_001003	4506668	602761378F1 cDNA, 5' end /clone=IMAGE:4896908 /clone_end=5'	1	GCAAAGAAAGAAAGATCCGAGGAGT CTGATGATGACATGGGCTTTGGTCT
7310	db mining	Hs.179661	BC008791	14250651	Homo sapiens, tubulin, beta 5, clone MGC:4029 IMAGE:3617988, mRNA, complete cds /cds=(1705,3039)	1	TTGAAAAGATGACATCGCCCCAAGAG CCAAAAATAATGGGAATTGAAAA
7311	db mining	Hs.179986	NM_005803	6552331	flotillin 1 (FLOT1), mRNA /cds=(184,1447)	1	TTTTCTGACCAAGACTGAGGGATGG GCTGGAGGTTTCAACTTTGCTACT
7312	db mining	Hs.180859	NM_016139	7705850	16.7Kd protein (LOC51142), mRNA /cds=(81,538)	1	TCTGGGACTGGGCAATGTTGTGTG GCCTCCTTAACTAGCTGTTATGT
7313	db mining	Hs.181301	AK024855	10437263	cDNA: FLJ21202 fis, clone COL00293 /cds=UNKNOWN	1	AACCTAAACGATTTTCACTCACTCTG GCTCCTTCTCCATAAAGCACATT
7314	db mining	Hs.181311	NM_004539	7262387	asparaginyl-tRNA synthetase (NARS), mRNA /cds=(73,1719)	1	CCACCAATGTCATGTCATGTAATTC AATAGGCTGTATTCAGAGCAGTCA
7315	db mining	Hs.181391	AL390158	9368848	mRNA; cDNA DKFZp761G2113 (from clone DKFZp761G2113) /cds=(0,564)	1	TGTACAGGTAGCTAATTTGTAAACG CTGTGATTTCCCTCTGCCCCCATG
7316	db mining	Hs.182281	NM_016407	7705482	hypothetical protein (HSPC164), mRNA /cds=(70,990)	1	TCTCATCATTTTCAAGATAGCAGAGT CATAGTTGGGCACCCAGTGATTGG

Table 8

7317	db mining	Hs.183180	NM_016476	13324711	anaphase promoting complex subunit 11 (yeast APC11 homolog) (ANAPC11), mRNA /cds=(0,398)	1	CAACAAGGTGGAAACAAGGGCTGGA GCTGCGTTTGTTCGCATCACTAT
7318	db mining	Hs.183593	NM_006965	5902161	zinc finger protein 24 (KOX 17) (ZNF24), mRNA /cds=(164,1270)	1	GAGCATTCTCAGGGGAGGTACCT GTGAGGTTCCCAGAACTGTAGTTTT
7319	db mining	Hs.184029	AL137509	6808164	Homo sapiens, clone MGC:2764 IMAGE:2958229, mRNA, complete cds /cds=(70,1785)	1	TGCAGGTGTGACAAGATCCGCCATC TGTAATGTCCTTGGCAACAATAAAA
7320	db mining	Hs.187652	AA833892	2907491	od64g04.s1 cDNA /clone=IMAGE:1372758	1	AAGAGTCTGACTTCTCACTAGGAGCA TGCTGTGTACTTACTTCAAACA
7321	db mining	Hs.188751	BG111638	12605142	602282682F1 cDNA, 5' end /clone=IMAGE:4369892 /clone_end=5'	1	CAAAACACCAAAACCAAGATAACACCGG AACGATAAACAGCAGAAACAGAGA
7322	db mining	Hs.193392	U46120	1184779	expressed unknown mRNA /cds=UNKNOWN	1	TGGGTTTGTCAGTTCAGGCTAGATG TGCATCATGGCAGGAAGAAAGAG
7323	db mining	Hs.195453	NM_001030	4506710	ribosomal protein S27 (metalloproteinase 1) (RPS27), mRNA /cds=(35,289)	1	AAGGATGTTCTTCAGGAGGAAGCA GCAGTAAAGCACTCTGAGTCAAGA
7324	db mining	Hs.196914	D86976	1504025	mRNA for KIAA0223 gene, partial cds /cds=(0,3498)	1	CGGAAGCCACCGTGTGGTCTTTCAC AGGCACGTTTATTTGCTGAAATA
7325	db mining	Hs.198281	NM_002654	4505838	pyruvate kinase, muscle (PKM2), mRNA /cds=(109,1704)	1	CCTCCACTCAGCTGTCTGCAGCAAA CACTCCACCCCTCCACCTTCCATT
7326	db mining	Hs.200317	AB037825	7243188	mRNA for KIAA1404 protein, partial cds /cds=(64,5841)	1	TCCCTCCTCCAGTGTCTTCTAGAAC AGACATTTAGGTATCTCAGTCCCT
7327	db mining	Hs.202613	BG284262	13035032	602407238F1 cDNA, 5' end /clone=IMAGE:4519449 /clone_end=5'	1	CAGCCGCAGCATCTAAACGAACA GAGGAGAACGACGAGGACAGATT
7328	db mining	Hs.210778	AL136679	12052881	mRNA; cDNA DKFZp564C1278 (from clone DKFZp564C1278); complete cds /cds=(104,1690)	1	TCACTGGATTCTGTGTCTTCACTAG AACACCATTTGCATCTCATATTGA
7329	db mining	Hs.211594	NM_006503	5729990	proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), mRNA /cds=(12,1268)	1	GCTTCTCTCGACCCCCAGCACCTCT GTCCCAAACCTCATTTCCCTTTTT
7330	db mining	Hs.226307	NM_004900	4758159	phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA /cds=(79,651)	1	AGCTGCTCAGACACACGAGCAAGC AATGTGCTCCTGATCAAGTAGATT
7331	db mining	Hs.326048	NM_006319	5453905	cDNA FLJ14186 fis, clone NT2RP2005726 /cds=UNKNOWN	1	ATGCTCATGTGGTGTCCCCACCGCC CACTTGTGTGATGTCACTGACTGTC
7332	db mining	Hs.227835	NM_014972	14149656	KIAA1049 protein (KIAA1049), mRNA /cds=(98,2126)	1	GCTGAGTGTGTCCTCCTCGTCCCA CTGTTTCTCTATAAATGTAAATGG
7333	db mining	Hs.231967	NM_014423	7656878	ALL1 fused gene from 5q31 (AF5Q31), mRNA /cds=(337,3828)	1	TGCAGCACATTGATAAGATGGTTTCC GTGAGCTATGATAAGATTGAAATT
7334	db mining	Hs.232400	NM_031243	14043071	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(169,1230)	1	ATAAATATGCAGTGATATGGCAGAG ACACCAGAGCAGATGCAGAGAGCC
7335	db mining	Hs.236131	NM_022740	13430859	homeodomain-interacting protein kinase 2 (HIPK2), mRNA /cds=(108,3704)	1	TTGAACCGGGAAGTGGGAGGACGTA GAGCAGAGAAGAGAATTTTAAA
7336	db mining	Hs.343558	AF090896	6690168	clone HQ0131 PRO0131 mRNA, partial cds /cds=(0,233)	1	TTTGCTCATTCTAAACTCAAGCTTTTA AGCCTCACAGAATTTACAGGGGT
7337	db mining	Hs.238936	BG538032	13530264	602563534F1 cDNA, 5' end /clone=IMAGE:4688193 /clone_end=5'	1	GCCATAGGCTTACATGGGCACTACTC GTTACACAGTCAGAAATGTTTGAAA
7338	db mining	Hs.241412	NM_030882	13562089	apolipoprotein L, 2 (APOL2), mRNA /cds=(477,1490)	1	GGTCTCTCGCTGTCTTCTCCAGCAT CCACTCTCCCTGTCTCTCTGGGG
7339	db mining	Hs.241471	AL133642	6599293	mRNA; cDNA DKFZp586G1721 (from clone DKFZp586G1721); partial cds /cds=(0,669)	1	TCAGCACCAGTCATGTTTAAAGAC CAGAGAGACAAGCATTTTGCCAAAG
7340	db mining	Hs.245188	NM_000362	9257248	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA /cds=(1183,1818)	1	CGAACCTGTCTAGAAGGAATGTATT TGTTGCTAAATTCGTAGCACTGT
7341	db mining	Hs.249170	NM_012476	7110734	ventral anterior homeobox 2 (VAX2), mRNA /cds=(32,904)	1	CAAAATGGCCTTGGTCCCGCAGCTTGT GTGCGTGAGTGCAGTGTGAGTGTG
7342	db mining	Hs.258551	NM_012100	6912247	aspartyl aminopeptidase (DNPEP), mRNA /cds=(151,1578)	1	CTCTTGGAAGACTTCTCTGCCATCC CTTTGCACCTGAGAGGGGAAGTTC
7343	db mining	Hs.259412	BG772376	14083029	602722490F1 cDNA, 5' end /clone=IMAGE:4839143 /clone_end=5'	1	GGCGCGGTGACCCACTTATGGGACT TGGCCTTTCTTTGTTGTTTAA
7344	db mining	Hs.259577	AW665292	7457838	hJ02c11.x1 cDNA, 3' end /clone=IMAGE:2980628 /clone_end=3'	1	ACCCAGTTTCATGATTACTTCTACTCT AACACTCAATCCGCCCTAATTAACCC
7345	db mining	Hs.259679	AW956608	8146291	EST368678 cDNA	1	TTCGATAAAGCAGGTTGACTTGCTTG TACCACCTTAAGAGTTGTGAGTGCT
7346	db mining	Hs.265827	NM_022873	13259549	interferon, alpha-inducible protein (clone IFI-8-16) (G1P3), transcript variant 3, mRNA /cds=(107,523)	1	TCCAGAACTTTGTCTATCACTCTCCC CAACAACCTAGATGTGAAACAGA
7347	db mining	Hs.265891	AK001503	7022798	cDNA FLJ10641 fis, clone NT2RP2005748 /cds=UNKNOWN	1	GGGATCTTTCAAATGGATAGTGAGTT GCCTTTCTATAGGTGACAATCA

Table 8

7348	db mining	Hs.266456	AW768693	7700715	hk65e11.x1 cDNA, 3' end /clone=IMAGE:3001580 /clone_end=3'	1	AGAGCAAGCATTACAGAAATAGGTC TGGAAACAGAGGAAAGGACAAAGA
7349	db mining	Hs.267368	NM_017842	8923451	hypothetical protein FLJ20489 (FLJ20489), mRNA /cds=(482,1201)	1	ATGTGTCTGCTGCCCTCAGCTCTTTGC CTTATCTGTGTCACTGTCACTTTA
7350	db mining	Hs.267812	NM_003794	4507144	sorting nexin 4 (SNX4), mRNA /cds=(0,1352)	1	TCCTGTGAATTGAATTTCTCTCAATC AAAGTGCCCCAAACAGAAAGCACA
7351	db mining	Hs.272027	NM_012177	6912365	F-box only protein 5 (FBXO5), mRNA /cds=(81,1404)	1	AGGTCCCTCGCTGGTACAAAGAAAA GCAAAAAGAATTTACGAAGATTGT
7352	db mining	Hs.272534	AL080068	5262475	mRNA; cDNA DKFZp564J062 (from clone DKFZp564J062) /cds=UNKNOWN	1	GCCAGAAGCATAATTTACCAGAGACG AGAACAGGGTGTGGGAGAGAGGAA
7353	db mining	Hs.273415	NM_000034	4557304	aldolase A, fructose-bisphosphate (ALDOA), mRNA /cds=(167,1261)	1	TCTTTCTCCCTCGTGACAGTGGTGT GTGGTGTCTGTCTGTCACTTAAG
7354	db mining	Hs.273830	AK022804	10434416	cDNA FLJ12742 fis, clone NT2RP2000644 /cds=UNKNOWN	1	CAGTCAAACATTTTACCTTGTGCCTT GGCTCACTCTGTGCCCTTTCTCCA
7355	db mining	Hs.274287	AK001508	7022805	cDNA FLJ10646 fis, clone NT2RP2005773, highly similar to pyroline 5-carboxylate reductase isoform mRNA /cds=UNKNOWN	1	ACAGGAAACGGGCTTTCTCTGAATTG GTAAATGGGAAAGAAGTGAGCAAC
7356	db mining	Hs.275163	NM_002512	4505408	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(72,530)	1	GTCCCTGGACACAGCTCTTCATTCCA TTGACTTAGAGGCAACAGGATTGA
7357	db mining	Hs.276818	AI435118	4300940	th95e09.x1 cDNA, 3' end /clone=IMAGE:2126440 /clone_end=3'	1	ACCCTCGCCACAAGATTCTGCAATCT CCTAAAGTACAGATGAGAAAGGAA
7358	db mining	Hs.278582	AF135794	4574743	AKT3 protein kinase mRNA, complete cds /cds=(0,1439)	1	TGCCAAGGGGTTAATGAAACAATAAG CTGTTGACGTTTGTCTCACTTTAAG
7359	db mining	Hs.279535	AK027035	10440049	cDNA: FLJ23382 fis, clone HEP16349 /cds=UNKNOWN	1	CAGTGGCACACCTTAACCACTCACTA ATTTTCACTGTTGTGAAAGTGATT
7360	db mining	Hs.283007	NM_008227	5453913	phospholipid transfer protein (PLTP), mRNA /cds=(87,1588)	1	CCCAGTGCCACAGAGAAAGACGGGAT TTGAAGCTGTACCCAATTTAATTCC
7361	db mining	Hs.283565	NM_005438	4885242	FOS-like antigen-1 (FOSL1), mRNA /cds=(34,849)	1	TGAGCCCTACTCCCTGCAGATGCCAC CCTAGCCAATGTCTCCTCCCTTC
7362	db mining	Hs.284296	AK026646	10439543	cDNA: FLJ22993 fis, clone KAT11914 /cds=UNKNOWN	1	GCAGGGAGGGGAGGATAAGTGGGAT CTACCAATTTGATTCTGGCAAAACAA
7363	db mining	Hs.284892	AF246229	10419514	AF246229 cDNA /clone=RB82	1	GGCCACTACCTTTGTTGAAACAAG CATAAGGGAGTGAAGTGTCTAAA
7364	db mining	Hs.284893	AF246230	10419515	AF246230 cDNA /clone=RB16	1	GCTGGCCGATCTCTCCCAAGATT GCAAGAAGCATTTCAGAAATAGT
7365	db mining	Hs.285280	AK024885	10437298	cDNA: FLJ21232 fis, clone COL00752 /cds=UNKNOWN	1	ATTGGGATGAAACTACTTTAGCAAAG TCCACAGATCAGAAACAGACGGT
7366	db mining	Hs.288038	NM_006625	12056474	TLS-associated serine-arginine protein 1 (TASR1), mRNA /cds=(72,623)	1	AGGAGACTGGGTGCTATAGTATTGATT ATTTTGAGGCAGACAGAGAGCTGT
7367	db mining	Hs.288283	AK026008	10438707	cDNA: FLJ22355 fis, clone HRC06344 /cds=UNKNOWN	1	AGCCTGCAAGGTTAGGACTTGAAGA GGGAAGGTATTTAATAACTGGGCGA
7368	db mining	Hs.289043	AL136719	12052856	mRNA; cDNA DKFZp566G0346 (from clone DKFZp566G0346); complete cds /cds=(278,790)	1	TTAGTGCAGTTGGAAATGAATGTGTAT AGGTCAGAGGTTCTCGTGTTCACA
7369	db mining	Hs.289087	AK024468	10440449	mRNA for FLJ00061 protein, partial cds /cds=(0,522)	1	TCACCTCTCAGTTGAAAGATTCTCTCT TTGAAAGGTCAAGACCTGTAAGT
7370	db mining	Hs.289494	BF475245	11544422	EST 003 cDNA, 5' end /clone_end=5'	1	AGTCTGGATGAAGGCCTGCCTCAAA GAGACACTAATGGGAGGGAACAAA
7371	db mining	Hs.290874	BE730505	10144599	601562627F1 cDNA, 5' end /clone=IMAGE:3832302 /clone_end=5'	1	AAAGGAAGAAGCACGATGCAACAG AAACAAGACGAGACAGAGTGAGCGA
7372	db mining	Hs.332403	NM_024113	13129129	hypothetical protein MGC4707 (MGC4707), mRNA /cds=(72,1087)	1	ACTGCTTCAAGTCTTGACCCCTTTGT GTCTAATAGCTAAACAACATGTG
7373	db mining	Hs.292998	AW972292	8162138	EST384381 cDNA	1	AACAATAGGAATAAGGTTACTTCAGC CTTAAGGGGCTTATCATACTGCTG
7374	db mining	Hs.293984	NM_032323	14150097	hypothetical protein MGC13102 (MGC13102), mRNA /cds=(161,1345)	1	GACAGGGAAATCTGCCTACCAAGAG GGGTGTGTGTGCTTTGTGCCCA
7375	db mining	Hs.295362	AK027365	14041993	cDNA FLJ14459 fis, clone HEMBB1002409 /cds=UNKNOWN	1	AACAAGTCCATGACTCCCAAGGGTTT AAGGACCAATGGTTCACTGAGACA
7376	db mining	Hs.297964	BF836049	12187621	RC1-HT0975-161100-011-g07 cDNA	1	ACACTCATCTCATATGTACGTGCTC AGTCGAACGGACTGCAGTCCGTTT
7377	db mining	Hs.299329	AK000770	7021066	cDNA FLJ20763 fis, clone COL09911 /cds=UNKNOWN	1	TACTGCTATGGAATGAGACCACCACT TCTCCTGTTGTCTCTCCAGCTTC
7378	db mining	Hs.300631	AK022958	10434851	cDNA FLJ12896 fis, clone NT2RP2004194, weakly similar to Rattus norvegicus Golgi SNARE GS15 mRNA /cds=UNKNOWN	1	TGCCAAGTGAGGACAACTGCTAGG CTGTATCCCATATTTTCAGGATGAG
7379	db mining	Hs.301417	M80899	178282	novel protein AHNK mRNA; partial sequence /cds=(0,3835)	1	AAACCGACCGCCTGTAGGCTCCTGG AACTATACAGATAGGTAAAGAGTTT
7380	db mining	Hs.301612	NM_005253	4885244	FOS-like antigen 2 (FOSL2), mRNA /cds=(3,983)	1	GACCAATCATCAGACTCCTTGAACCT CCCACCTCTGCTGGCTCTGTAACC
7381	db mining	Hs.301636	NM_000287	4505728	peroxisomal biogenesis factor 6 (PEX6), mRNA /cds=(70,3012)	1	AGAGATCCAGGTGCTAAGTGGATTGA GACAGCAGCAACAGCTCAAGAGATA

Table 8

7382	db mining	Hs.337774	NM_004723	4758671	rho/rac guanine nucleotide exchange factor (GEF) 2 (ARHGEF2), mRNA /cds=(112,2988)	1	ATGTCCCTTTCTCCTCTCCCTCTTC CTCTTACTGCTGTCTCCCTTTCT
7383	db mining	Hs.318568	BF475243	11544420	EST 001 cDNA, 5' end /clone_end=5'	1	ACATCCATAGAACAAATACATCAAAAGT TGTTGAAGTGTTCAGGGGAGGGC
7384	db mining	Hs.318569	BF475244	11544421	EST 002 cDNA, 5' end /clone_end=5'	1	AGCACTTACTGTCAGGCATTCAGAAAT GTGAGCAATGACAATAATTTACCT
7385	db mining	Hs.321709	NM_002560	4505548	purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA /cds=(27,1193)	1	AATCTGATTGAGTCTCCACTCCACAA GCACTCAGGGTTCCCGCAGCTC
7386	db mining	Hs.322478	D38491	559327	mRNA for KIAA0117 gene, partial cds /cds=(0,683)	1	AACCCAAGAAAAGAGTTGCTCTTACT ATCTACTGCTGACTCTTGAACCTT
7387	db mining	Hs.323114	AK023846	10435906	cDNA FLJ13784 fis, clone PLACE4000593 /cds=UNKNOWN	1	TTCTAGGTGGGCTTTTCCTATCAGA GCTTGGCTCATACCAAAATAAGT
7388	db mining	Hs.323949	NM_002231	13259537	kangal 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1), mRNA /cds=(181,984)	1	AGGTGGGCTGGACTTCTTACGCCCC TCAAGGGTGTGTATATTGTATAGGG
7389	db mining	Hs.324507	NM_024524	13375667	hypothetical protein FLJ20988 (FLJ20988), mRNA /cds=(182,2056)	1	TGTGTGCAATGGCACTAGTTCAGTT TATGTCCCTTCTGATATAGTAGCT
7390	db mining	Hs.326447	BC004857	13436058	Homo sapiens, clone IMAGE:3690478, mRNA, partial cds /cds=(0,71)	1	CTATCAGCCCCAAGTGAGCAGAAC AGAGGGATTGGAGCAAGTGTCTCTC
7391	db mining	Hs.333558	BG577468	13592532	gu.seq cDNA	1	TGCTAAGGAGAGGGGCCATGAAGAG TTTTGTTGAGAACATCGTGTCTGAG
7392	db mining	Hs.334303	BG642392	13777102	gu.seq395250 cDNA	1	AGTCAGAACTTCAAGTCCCATTAATA GGGGCTGGAAATACAAGTACAGT
7393	db mining	Hs.334804	NM_000558	6715603	hemoglobin, alpha 1 (HBA1), mRNA /cds=(37,465)	1	CTCCCTTCTGTCACCGCTACCCCC GTGGTCTTTGAATAAAGTCTGAGTG
7394	db mining	Hs.334853	NM_032241	14149953	hypothetical protein FLJ23544 (FLJ23544), mRNA /cds=(125,517)	1	CAGATGGTGTGGGGTCAAGTACATC CCAGTCGTGGCCCTTTGGACAAG
7395	db mining	HS.250655	NM_032695	14249283	Prothymosin, alpha (gene sequence 28)	1	TTTTGGCCTGTTGATGTATGTGTGA AACAATGTTGTCCAACAATAAACA
7396	db mining	Hs.336689	AA493477	2223318	ESTs	1	AGCCTAGGTGACAGAGCAAGACTCC ATTTCAAAAACAAAACAAAACAAA
7397	db mining	Hs.180450	BF791433	12096487	ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(37,429)	1	ACACTGAGAATACAGCATACACGC ACGCACAAGACAACAACATACAGC
7398	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	1	CAGCCACCTCCTCAGGTGAGACAAG CCCAGCACCCAATACCCTATCTG
7399	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:928806 similar to contains Alu repetitive element, mRNA	1	GGCTTCCCTATTACCTCCCAGCGAAA TTCGTAGTCTTTCTCTATGGAGTT
7400	Table 3A	NA	AA501934	2236901	nh56a10.s1 NCI_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	1	TGCTGATGTGTTAGGTAGTTGTGGCA CACTCACCTGTCTTCTCTAAATGC
7401	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCI_CGAP_Pr1 cDNA clone IMAGE:915581 similar to contains Alu repetitive element; contains	1	TTCTGCTCAGCAAAACAACGTTTAA GGATGGTGAGAGAAGACAAAGTAA
7402	Table 3A	NA	AF249845	8099620	isolate Siddi 10 hypervariable region I, mitochondrial sequence	1	TATTAACCACTCACGGGAGCTCTCCA TGCATTTGGTATTTTTCGTCTGGGG
7403	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	1	TTACCTGCTTTGCATGCTCTCCATCG TCAAAGTCTTCTGGAACTTAGGC
7404	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	1	CCCCACCACCAACATACAAAGCTTT CCCACCAATCCTTGAAGTCAAAA
7405	db mining	NA	AI732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element, mRNA s	1	TTCAAGGTCCCAATACCAACTAACT CGAAGGAAGAAATGGAATCTATT
7406	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	1	TGCACAGAACTCTTACTTACATGTCT CATCGAAACTCCAGAACCCGTCG
7407	Table 3A	Hs.232000	AW380881	6885540	UI-H-BI0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	1	TGCATGTATCCCGGTAAATCAAATCC AATTCACAGCCACTGCTGAATAT
7408	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	1	TACAGGAAAATGAAACTAGACGGGTG GGGGACACTAGAATGAAAACCACT
7409	Table 3A	NA	AW836389	7930363	PMO-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	1	AGTTTCTGCTTTCAGTGACTGAGGCT TTGCTTTAACCTGGTGACTCCCA
7410	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	1	TCCCACCTCAAGTTAAGCACCAAGC AATCACTAATCTGGAGCAGAGGA
7411	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	1	CATGGATGGGGGCGAGTGGTGTCTCT AGTGTGTGAGGAAGCAGAGCAGATG
7412	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	1	TCACCACAGATGGGAAGATCGTTTCC TGAAAACAGTCTATAAATACAGAG
7413	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	1	CAGACGCTCCAGTGCTGCCGAGGTT AGTGTGTTTATTAGACCTGAAATGA

Table 8

7414	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	1	CCCTTTAGGCCTCTTGCCCGAACAGT GAACACTAATAGATATCCTAAGCT
7415	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	1	ATGGGGATCATGTTTATTTTCTCTA TATAATGGGCGAGTGTGTCCCA
7416	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	1	AGCTGTAGACCATAGCCACCTTCAG GTAGTGGTTTGGGAAATCAAGCAA
7417	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	1	TGTACTTATGCTTGTCTTCTACCTG CCCCAGTCTTGAAGTGGTGGA
7418	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	1	GGAGGGTGTGGGAAGCAAGAGAAGA ACATTCTGTTAGGGGAGAGAAGAA
7419	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1822)	1	GCATCTCCAGCTTTCATAGTTACCCA ACTGTAAACCAGAGATGTGCTG
7420	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	1	GGCCAGTGCCAGACGGTAGCTAGTT GGATGCTAAGGTTAGAATTTAGATA
7421	Table 3A	Hs.301497	BE168334	8631159	arginine-IRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	1	GGCATTGTAGGTTGACACGACGAAAG ACTCAGAGTGACTTGAGCATTGGA
7422	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	1	AGCCCATTTGGATATGGCCCATCTTT ACCTAATGGCTACTATAGTAGGTT
7423	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	1	AATCAGCAGTAGTAAGTCCAGTAGGA AAGATTCTCAAAGGAATAGTTCTT
7424	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	1	AATGGTCAGGCACAGGTAGATCAAA GTCTGTATGTATGTTACACAGA
7425	Table 3A	NA	BE247056	9098807	TCBAP1D6404 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA cDNA clone T	1	TACCTGAAGGTGTAGAGAGTGCCCG CATCCAGCAAGGCCAACAGCTCCAC
7426	Table 3A	Hs.11050	BE763412	10193336	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	1	CTGTGTTTTCCCAAAGCAACAATTTT AAACAAAGTGAGAGCCACTGACA
7427	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	1	GACTCCGAGCTCAAGTCACTGTGTAC CCCCACCCCTAACCCACTGCATC
7428	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	1	TGTAAGTCACTTTATGTATCACTCAAG TCTTGCCCTTACTGAGTGCCTGA
7429	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	1	TCTCTCTAACCAAACTGTAATCTTCA GGACAGCAAACTCAGCCCAAGG
7430	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	1	AACCTCTGGTTAAATGGGTTAATAGA GGATTGGAACACTTTGTTGCTGT
7431	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	1	AGAAGCAAACCTGTGAAGCTACTATC GTTTATCATCAGTGTGAATGCAT
7432	Table 3A	NA	BF749089	12075765	MR2-BN0388-051000-014-b04 BN0388 cDNA, mRNA sequence	1	GGACTAACTTCCACCTCTCTGCTAC TTCCAGCTGCTCTTAATCACACTT
7433	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	1	AGTCTTCCACCCAGCATAGGTATCAC ACAACCAAGCTCTGTTTTTCTCTG
7434	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	1	TTAGCTGGTACATTGTTTCAAGTTTA CTGGGAGCCGGTAAGATAGTCAAC
7435	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	1	AGCGTGATGCTTCCCTCATGTCCGTGA TTTTCTGTGAGACATCTTCAAGC
7436	Table 3A	NA	BF805164	12134153	QV1-CI0173-061100-456-f03 CI0173 cDNA, mRNA sequence	1	ACAAAAGTATGGAATTCATTCTTTT ATATGCTGCAGCGATGTTCTGCCCT
7437	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	1	AGA TGTAATTGATTCCGCATAAACGGTTC ATTACTGGCACCTATGGCAGACC
7438	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	1	GTGATCCACTTGGAGCTGCTACTGGT CCCATTGAGTCTATAGTACTTCA
7439	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	1	TGCCATGAAATCTCTATTAACTCTCAG AAAGATCAAAGGAGGTCCCGTGT
7440	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	1	CCCACCTGGCAAATCCTCAAGTGTGA CCCTAGTCATCTTCTCCCTTTTGG
7441	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	1	GCTAAACAGAAAAGAACCTGAAGTAC AGTTCCTGCTTCAAAGAAGATGC
7442	Table 3A	NA	BF877979	12268109	MR0-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	1	ATCCTCCTCCCTGGGATGGCATAGA AGAGACTTTAAACCAAATGAGCC
7443	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	1	GTCAGTAAGCTCTGCCTGCCAAGAAG ACACAGTGAGAGGTGCCAGATGC
7444	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	1	GTTTCCACTAGTACTTCTTCTCTACC TGCTGTGAAGCTCTGCACCCCTGC
7445	Table 3A	NA	BF899464	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	1	AGAGTAATCCAGATCCAGGGGACAGT CACAATGACTACGGCTTTAGCTG
7446	Table 3A	Hs.324473	BF904425	12295884	40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	1	GCAGGGCTACACCAAGTCCATTGATA TTTGGTCTGTAGGTTCCAGATCTGG
7447	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	1	TCTTCTCTAAATGCCTCTCTCTCTT CCTTTTCCAGACCTGGTTTAAA
7448	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, clone MGC:18218 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	1	TGCGCATTTGGTAGGTTCCAGATGAC TGCTCTTCTATTTACGAAGCCAC
7449	Table 3A	Hs.75703	BF928844	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	1	GTAGATTACTATGAGACCAGCAGCCT CTGCTCCCAGCCAGCTGTGGTGTG

Table 8

7450	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	1	TTTCCTTTTCGCTGACTTTCTCACTCA CTGTCTGTCTCTCATTTTCTCCA
7451	Table 3A	NA	F11941	706260	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	1	TGGTAAGTTTTCGGCAGTGTGGAGAC AGGGGAATAATCTCAACAGTAGGT
7452	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 89881 cDNA clone xs425, mRNA sequence	1	CCATGGTGGTGCTTGACTTTGCTTTG GGGCTTAATCCTAGTATCATTTGG
7453	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	1	TCAGTGGGTGTTGGTTGTCCATTAGT TGAGACTTAGTTGTTGCTCTGGGA
7454	Table 3A	NA	W27656	1307658	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	1	GGCTGGACAGCAGATGATTCAAATCT CAATACTACATGCCATTTCTGTGG
7455	literature	NA	X17403	59591	Human cytomegalovirus strain AD169 complete genome	1	AATAATAGATTAGCAGAAGGAATAAT CCGTGCGACCGAGCTTGTGCTTCT
7456	literature	NA	X17404	59591	Human cytomegalovirus strain AD169 complete genome	1	TTTTGCGAACTTTTAGGAACAGCAA GTCAACAAAAGACTAACAAAGAAA
7457	literature	Hs.2799	X17405	59591	Cartilage linking protein 1	1	GAGATCGACATCGTCATCGACCGAC CTCCGCGAACCCCTACCCAATCC
7458	literature	Hs.2159	X17406	59591	mRNA for cartilage specific proteoglycan	1	ACATTCAAAGTTTGAGCGTCTTCAT GTACGCCGTTTTCGGCCCTCACGAG
7459	literature	NA	X17407	59591	Human cytomegalovirus strain AD169 complete genome	1	CCAACGACACATCCACAAAAATCCCC CATCGACTCTCACAATCGCATCAT
7460	literature	NA	X17408	59591	Human cytomegalovirus strain AD169 complete genome	1	CTTTGAGCAGGTTCTCAAGGCTGTAA CTAACGTGCTGTCCGCCGCTTTTC
7461	literature	NA	X17409	59591	Human cytomegalovirus strain AD169 complete genome	1	GATGTCCGCTACCGGCTATCGGCC ATCATCGGCATCTATCTGCTCTACC
7462	literature	NA	X17410	59591	Human cytomegalovirus strain AD169 complete genome	1	TCTTCTGGGACGCCAACGACATCTAC CGCATCTTCGCCGAATTGGAAGGC
7463	literature	NA	X17411	59591	Human cytomegalovirus strain AD169 complete genome	1	ACGAACAGAAATCTCAAAGACCTG ACCCGATAAGTACCGTACCGGAGA
7464	literature	NA	X17412	59591	Human cytomegalovirus strain AD169 complete genome	1	AGAGAACACAAACCACACGACGA TGAAACAAACCGTCAACCAACA
7465	literature	NA	X17413	59591	Human cytomegalovirus strain AD169 complete genome	1	CTGCATCGTCGTCCTCTCTCTCTCT CGGAGATCGCGACGGAGAAACAAC
7466	literature	NA	X17414	59591	Human cytomegalovirus strain AD169 complete genome	1	CTGAGCCTGGCCATCGAGGCAGCCA TCCAGGACCTGAGGAACAAGTCTCA
7467	literature	NA	X17415	59591	Human cytomegalovirus strain AD169 complete genome	1	CCTCTGGAGGCAAGAGCACCCACCC TATGGTGACTAGAAGCAAGGCTGAC
7468	literature	NA	X17416	59591	Human cytomegalovirus strain AD169 complete genome	1	TTGCTGGGACCAAGTTTCGAAGAA CTACACTGTCTGTGGCCGAGTTT
7469	literature	NA	J01917	209811	Adenovirus type 2, complete genome	1	CTGTGGAATGTATCGAGGACTTGCTT AACGAGTCTGGGCAACCTTTGGAC
7470	literature	NA	J01918	209811	Adenovirus type 2, complete genome	1	GCTGGCCGTGACCCCGCGGAGTTT GGCTCTAGCGATGAAGATACAGATT
7471	literature	NA	J01919	209811	Adenovirus type 2, complete genome	1	GGGGCGGTTAGGCTGTCTCTCTCTCT CGACTGACTCCATGATCTTTTCTG
7472	literature	NA	J01920	209811	Adenovirus type 2, complete genome	1	TGTTTGCCTATTATTATGTGGCTTAT TTGTTGCCTAAAGCGCAGACGCG
7473	literature	Hs.250596	J01921	209811	xy45f10.x1 cDNA, 3' end /clone=IMAGE:2856139 /clone_end=3'	1	ACGGTGATCAATAAAGCTATGTGGT GGTGGGGCTATACTACTGAATGAA
7474	literature	NA	J01922	209811	Adenovirus type 2, complete genome	1	TTTCTGCCCTGAAGGCTTCTCTCCCT CCCAATGCGGTTTAAACATAAAAT
7475	literature	NA	J01923	209811	Adenovirus type 2, complete genome	1	GGCTTATGCCCATGTATCTGAACATC CAGAGTCACTTTTACCAGTCTGTG
7476	literature	NA	J01924	209811	Adenovirus type 2, complete genome	1	CTACTGCCGTACAGCGAAAGCCGCC CCAACCCGCGAAACGAGGAGATATG
7477	Table 3A	NA	AA077131	1836605	7B08E10 Chromosome 7 Fetal Brain cDNA Library cDNA clone 7B08E10, mRNA sequence	-1	CAGATAGTGGTATTTGGGTGTGGG CTTGCTGACCTGAGGAGGTGGCTG
7478	Table 3A	NA	AA501725	2236692	ng18e12.s1 NCL_CGAP_Lip2 cDNA clone IMAGE:929806 similar to contains Alu repetitive element, mRNA	-1	AACTCCATAGAGAAAGACTACGAATT TCGCTGGGAGGTAATAGGGAAGCC
7479	Table 3A	NA	AA501834	2236901	nh56a10.s1 NCL_CGAP_Pr8 cDNA clone IMAGE:956346, mRNA sequence	-1	GCATTTAGGAAAGACAGGTGAGTGTG CCACAACCTACCTAACACATCAGCA
7480	Table 3A	NA	AA579400	2357584	nf33d05.s1 NCL_CGAP_Pr1 cDNA clone IMAGE:915561 similar to contains Alu repetitive element; contains	-1	TTACTTTGTCTTCTCTCACCATCCTAA AACGTTGTTTGTCTGAGCATGAA
7481	Table 3A	NA	AF249845	8099620	Isolate Siddi 10 hypervariable region I, mitochondrial sequence	-1	CCCCAGACGAAAATACCAATGCATG GAGAGCTCCCGTGAGTGGTTAAATA
7482	db mining	Hs.277051	AI630242	4681572	ad07c09.y1 cDNA /clone=ad07c09- (random)	-1	GCCTAAGTTTCCAGAAGACTTTGACG ATGGAGAGCATGCAAGCAGGTAA
7483	db mining	Hs.277052	AI630342	4681672	ad08g11.y1 cDNA /clone=ad08g11- (random)	-1	TTTGGCAGTTCAAGGATTGGTGGGAA ACGTTTGTATGTGTTGGGGTGGGG

Table 8

7484	db mining	NA	AJ732228	5053341	nf19e05.x5 NCI_CGAP_Pr1 cDNA clone IMAGE:914240 similar to contains Alu repetitive element; mRNA s	-1	AATAGATTTCATTTCCTTCCTCGAGT TAGTTGGGTATTGGGACCTTGAA
7485	Table 3A	Hs.197803	AW379049	6883708	mRNA for KIAA0160 gene, partial cds /cds=(0,2413)	-1	CGACGGTGTCTGGAGTTTCGATGAG ACATGTAAGTAAGAGTTCTGTGCA
7486	Table 3A	Hs.232000	AW380881	6885540	UI-H-BI0p-abh-h-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2712035 /clone_end=3'	-1	ATATTGACAGTGGCTGTGAAATTGG ATTTGAATTACCGGGATACATGCA
7487	Table 3A	Hs.325568	AW384988	6889647	602386081F1 cDNA, 5' end /clone=IMAGE:4514972 /clone_end=5'	-1	ACTGGTTTTCTATTCTAGTGTCCCCCA CCCGTCTAGTTTCATTTCTCTGTA
7488	Table 3A	NA	AW836389	7930363	PM0-LT0030-101299-001-f08 LT0030 cDNA, mRNA sequence	-1	TTGGGAGTCACCAGGTTAAAGCAAAG CCTCAGTCACTGAAAGCAGAACT
7489	Table 3A	NA	AW837717	7931691	CM2-LT0042-281299-062-e11 LT0042 cDNA, mRNA sequence	-1	TCCTGTGCTCCAGAATTAGTGATTGC TTTGGTGTCTAACTTGAAGTGGGA
7490	Table 3A	NA	AW837808	7931782	CM1-LT0042-100300-140-f05 LT0042 cDNA, mRNA sequence	-1	CATCTGCTGTGCTTCTCCTCACACACTA GAAACACCACTGCCCCATCCATG
7491	Table 3A	NA	AW842489	7936472	PM4-CN0032-050200-002-c11 CN0032 cDNA, mRNA sequence	-1	TCTGTGATTTATAGACTGTTTTCAGGA AACGATCTTCCCATCTGTGGTGA
7492	Table 3A	NA	AW846856	7942373	QV3-CT0195-011099-001-c09 CT0195 cDNA, mRNA sequence	-1	TCATTTCAAGGTCTAATAAACACACTAA CCTCGGCAGCACTGGAGCGTCTG
7493	Table 3A	NA	AW856490	7952183	PM4-CT0290-271099-001-c04 CT0290 cDNA, mRNA sequence	-1	AGCTTAGGATATCTATTAGTGTTCACCT GTTCCGGCAAGAGGCTAAAGGG
7494	Table 3A	NA	AW891344	8055549	PM2-NT0079-030500-001-a04 NT0079 cDNA, mRNA sequence	-1	TGGGAACACACTGGCCCATATATAG AGAAAAATAAAACATGATCCCCAT
7495	Table 3A	NA	BE061115	8405765	QV0-BT0041-011199-039-f09 BT0041 cDNA, mRNA sequence	-1	TTGCTTGATTTCCAAACCACTACCT GAAGGTGGCTTATGGTCTACAGCT
7496	Table 3A	NA	BE086076	8476469	PM2-BT0672-130400-006-h09 BT0672 cDNA, mRNA sequence	-1	TTCCACCACTTCAAGACTGGGGGCA GGTAGAGAAGACAAGCATAAGTACA
7497	Table 3A	NA	BE091932	8482384	IL2-BT0733-130400-068-C11 BT0733 cDNA, mRNA sequence	-1	TTCTTCTGCCCCCTAACAGAAATGTT CTTCTCTGCTTCCCAACCCCTGC
7498	Table 3A	Hs.173334	BE160822	8623543	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA /cds=(0,1922)	-1	CAGCACATCTTCTGGTTACAAGTTG GGTAACATGAAAGCTGGAGATGC
7499	Table 3A	NA	BE163106	8625827	QV3-HT0457-060400-146-h10 HT0457 cDNA, mRNA sequence	-1	TATCTAAATTCTACCTTTAGCATCCAA CTAGCTACCGTCTGGCACTGGCC
7500	Table 3A	Hs.301497	BE168334	8631159	arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds /cds=(0,1544)	-1	TCCAATGCTCAAGTCACTCTGAGTCT TTGCTGGTGTCAACCTACAATGCC
7501	Table 3A	Hs.172780	BE176373	8639102	602343016F1 cDNA, 5' end /clone=IMAGE:4453466 /clone_end=5'	-1	ACCTCACTATAGTAGCCATTAGGTAA AGATGGGCCATATCCAAATGGGCT
7502	Table 3A	NA	BE177661	8656813	RC1-HT0598-020300-011-h02 HT0598 cDNA, mRNA sequence	-1	AAGAACTATTCTTTGAGAATCTTTCC TACTGGGAGTTACTGCTGTGATT
7503	Table 3A	NA	BE178880	8658032	PM1-HT0609-060300-001-g03 HT0609 cDNA, mRNA sequence	-1	TCTGTGTGAACATACATACAGGACTT TGATTCTACCTGTGCCTGACCATT
7504	Table 3A	Hs.86543	BE247056	9098807	602495247F1 cDNA, 5' end /clone=IMAGE:4809330 /clone_end=5'	-1	GTGGAGCTGTTGGCCTTGTGGATG CGGGCACTCTCACTTACAGTA
7505	Table 3A	Hs.11050	BE763412	10193336	mRNA; cDNA DKFZp434C0118 (from clone DKFZp434C0118); partial cds /cds=(0,1644)	-1	TGTCAGTGGCTCTCACTTTGTTTGA ATTGTTGCTTTGGGAAAAACACAG
7506	Table 3A	NA	BF330908	11301656	RC3-BT0333-310800-115-f11 BT0333 cDNA, mRNA sequence	-1	GATGCAGTGGGTTAGGGGTTGGGGG TACAGACTGACTTGAGCTCGGAGTC
7507	Table 3A	NA	BF357523	11316597	CM2-HT0945-150900-379-g06 HT0945 cDNA, mRNA sequence	-1	TCAGGCACCTCAGTAAAGGCAAGACTT GAGTGATACATAAAGTCAGTTACA
7508	Table 3A	NA	BF364413	11326438	RC6-NN1068-070600-011-B01 NN1068 cDNA, mRNA sequence	-1	CCTTGGGCTGAGTTTGTGGTCTCTGA AGATTACAGTTTTGGTTAGAGAGA
7509	Table 3A	NA	BF373638	11335663	MR0-FT0176-040900-202-g09 FT0176 cDNA, mRNA sequence	-1	ACAGCAAACAAAGTGTCCAATCCTC TATTAACCCATTTAACCAAGAGTT
7510	Table 3A	NA	BF740663	12067339	QV1-HB0031-071200-562-h04 HB0031 cDNA, mRNA sequence	-1	AGTGCACTTCACTGATGATAAACGA TAGTAGCTTCACAGGTTTGCTTCT
7511	Table 3A	NA	BF749089	12075765	MR2-BN0386-051000-014-b04 BN0386 cDNA, mRNA sequence	-1	AAGTGTGATTAGAAGCACTGGAAGT AGCAGAGGAGGTGGAAGTTAGTCC
7512	Table 3A	NA	BF758480	12106380	MR4-CT0539-141100-003-d05 CT0539 cDNA, mRNA sequence	-1	CAGGAGTAAACAGAGCTGGTTGTGT GATACCTATGCTGGGTGGAGACT
7513	Table 3A	NA	BF773126	12121026	CM3-IT0048-151200-568-f08 IT0048 cDNA, mRNA sequence	-1	GGTGACTATCTTACCGGCTCCAGTA AACTCTGAACAATGTACCAGCTAA
7514	Table 3A	NA	BF773393	12121293	CM2-IT0039-191200-638-h02 IT0039 cDNA, mRNA sequence	-1	GCTTGAAGATGTCTCAACAGAAATC ACCGACATGAGGAAGCATCACGCT
7515	Table 3A	NA	BF805164	12134153	QV1-CI0173-081100-456-f03 CI0173 cDNA, mRNA sequence	-1	TCTAGGGCAGGAACATGGCTGCAGC ATATAAAAAAGAAATTGAATCACTT TTGT
7516	Table 3A	NA	BF818594	12156027	MR3-CI0184-201200-009-a04 CI0184 cDNA, mRNA sequence	-1	GGTGTGCCATAGGTGCCAGTAATG ACCGTTTATGCGGAAATCAATTACA
7517	Table 3A	NA	BF827734	12171909	RC6-HN0025-041200-022-F08 HN0025 cDNA, mRNA sequence	-1	TGAAGTACTATAGGACTCAATGGGAC CAGTAGCAGCTCCAAGTGGATCAC
7518	Table 3A	NA	BF845167	12201450	RC5-HT1035-271200-012-F08 HT1035 cDNA, mRNA sequence	-1	ACACGGGACCTCCTTTGATCTTCTG AGAAATTAATAGAGATTCATGGCA

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7519	Table 3A	NA	BF869167	12259297	IL5-ET0119-181000-181-b11 ET0119 cDNA, mRNA sequence	-1	CCAAAAGGAGAAAGATGACTAGGGT CACACTTGAGGATTTGCCAGGTGGG GCATCTTCTTTGAAGACGGGAAGTGT ACTTCAGGTCTTTCTGTGTTAGC
7520	Table 3A	NA	BF875575	12265705	QV3-ET0100-111100-391-c02 ET0100 cDNA, mRNA sequence	-1	GGCTCATTGGGTTTTAAAGTCTCTTCT ATGCCATCCCAGGGGAGGAGGAT GACTGTGGACACCTCTCACTGTGTCT TCTTGGCAGGCAGAGCTTACTGAC
7521	Table 3A	NA	BF877979	12268109	MRO-ET0109-171100-001-b02 ET0109 cDNA, mRNA sequence	-1	GCAGGGTGACAGAGCTTCACAGCAGG TAGGAAGAAGTAACTAAGTGGAAC
7522	Table 3A	NA	BF897042	12288501	IL2-MT0179-271100-254-C11 MT0179 cDNA, mRNA sequence	-1	CAGCTAAAGCCGTAGGTCAATTGTGAC TGTCCTGGGATGTGGATTACTCT CCAGAATGCAGCCTACAGACCAATA TCAATGGAGCTTGGTGTAGCCCTGC
7523	Table 3A	NA	BF898285	12289744	QV1-MT0229-281100-508-e11 MT0229 cDNA, mRNA sequence	-1	TTTAAACCAGGTCTGGAAAAGGAAG GAGAGGAGGGCATTTTAGAGAAGA GTGGCTTCGTAATAAGAGCAGT CACTGTGGAACACCAATGGCGA
7524	Table 3A	NA	BF899484	12290923	IL5-MT0211-011200-317-f03 MT0211 cDNA, mRNA sequence	-1	CACACCACAGCTGGCTGGGAGCAGA GGCTGCTGGTCTCATAGTAATCTAC
7525	Table 3A	Hs.324473	BF904425	12295884	40 kDa protein kinase related to rat ERK2 /cds=(134,1180)	-1	TGGAGAAAATGAGAGACAGACAGTG AGTGAGAAAGTCAGCGAAAAGGAAA
7526	Table 3A	NA	BF906114	12297573	IL3-MT0267-281200-425-A05 MT0267 cDNA, mRNA sequence	-1	ACCTACTGTTGAGATTATCCCTGT CTCCACACTGCCAGAACTTACCA
7527	Table 3A	Hs.104679	BF926187	12323197	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds /cds=(2206,2373)	-1	CCAAATGATACTAGGATTAAGCCCCA AAGCAAAGTCAAGCACCACCATGG
7528	Table 3A	Hs.75703	BF928644	12326772	small inducible cytokine A4 (homologous to mouse Mip-1b) (SCYA4), mRNA /cds=(108,386)	-1	TCCCAGAGCAACAATAAGTCTCAAC TAATGGACAACCAACCCACTGA CCACAGAATGGGCATGTAGATTGAG ATTTGAATCATCTGCTGCCAGCC
7529	Table 3A	NA	BG006820	12450386	RC4-GN0227-271100-011-d03 GN0227 cDNA, mRNA sequence	-1	TACTGGCGTCGAGCCCACTGCCTCA GAAGACTTCCTTCATCTGTTCTCA
7530	Table 3A	NA	F11941	706280	HSC33F051 normalized infant brain cDNA cDNA clone c-33f05, mRNA sequence	-1	GTTTCAAGGGACATCTTCAGAGCCAA CATCTACCTCGGGGCTTTGTGAA CTACAGTTCTACCACTAAGCACTAGT CCCCCTGTACTTCCCTGCACAGGA TAGTTGCATGTGACAACAGAGATCAA CGACGAGACCCTCCACAGTATCCG
7531	Table 3A	NA	U46388	1236904	HSU46388 Human pancreatic cancer cell line Patu 8988t cDNA clone xs425, mRNA sequence	-1	TTGACCATAGAATCAAGCCTGAGGCT GTGAAGATGGTGAAGTGTGGAGA CTGCTGTCTTACCCGAATCTCCCAT TACCGGCCCTGGATCAACCAAGATC GTCACTGGAGGACCAACCCCTGCTG TCCAAAACACCACTGCTTCTTACCC CATGCCATGCATATTTCAACTGGGCT GTCTATTTTTGACACCAGCTTATT
7532	Table 3A	NA	U75805	1938265	HSU75805 Human cDNA clone f46, mRNA sequence	-1	GAGAAGCACCTCAACCTGGAGACAAT TCTACTGTTCAACAGCAGCAGCA ACTTGTGAGGGCCATTCTCTCCGG GCACTGGGTCACTAGGACTGTTTT GACAGCGTCTAGAAACCCTGGCGA, CCATTGCCTCCAGCGGGATAGAGTG CATCCTCTGGAGCCTGACCTGTGATC GTCGCATCATAGACCGCCAGTAGA GCCTCCACACGACATCACACCATATA CCGCAAGGAATATCAGGGATGCTG ACAGCCATCCTCCCTTGAGAGTCAT CAGAAAAATACATTAGGAAATGT ACCITTCGTCTTCTGAGTCTCATGCCT CAAAACCTAGTTTGATAGACAGGA AGATGGCTACCTCTCTGATTATGATC CTTTCGTAGAAAATGCTCAAACT ATGCATCGCCGACAAGTCTTGAAATTA GGATTGTCGAAATAGACAAAGAA CGGGTGTGTTCAATCATCGACGGTGA CAATCCTATCTCCATCTATAATCC GAAGAGCGAAATGCAATCTTCTGCTT CTTCACTAGAGACTTTACAGTCTT GCACATCCATCGCCCAAGTGAAGTC TGCAAGGATGCCATTTATTGGTTG TCTCGGTTTACCTTTTGTGTTGTG GTTCTTTGTTCTTGTGTTGTTGCT
7533	Table 3A	NA	W27656	1307858	36f10 Human retina cDNA randomly primed sublibrary cDNA, mRNA sequence	-1	
7534	literature	Hs.99962	BC005929	13543541	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein) (PRG2), mRNA /cds=(857,1525)	1	
7535	literature	Hs.46295	X14346	31182	eosinophil peroxidase (EPX), mRNA /cds=(0,2147)	1	
7536	literature	Hs.1256	J05225	179076	arylsulfatase B (ARSB), mRNA /cds=(559,2160)	1	
7537	literature	Hs.728	M28129	556208	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA /cds=(71,556)	1	
7538	literature	Hs.889	NM_001828	6325464	Charot-Leyden crystal protein (CLC), mRNA /cds=(33,461)	1	
7539	literature	Hs.135826	M89138	180539	chymase 1, mast cell (CMA1), mRNA /cds=(0,743)	1	
7540	literature	Hs.334455	NM_003293	13699841	trypsin, alpha (TPS1), mRNA /cds=(17,844)	1	
7541	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7542	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7543	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7544	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7545	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7546	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7547	literature	Hs.279852	BC004555	13528716	G protein-coupled receptor (G2A), mRNA /cds=(900,2042)	1	
7548	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7549	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7550	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7551	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7552	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7553	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	
7554	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	

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7555	literature	NA	NC_001345	9625578	Human herpesvirus 4, complete genome	1	TCTGAATACTCTACAAAACGCTCCTTGTCTGCTCTTAAACCATCTGTGT
7556	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TGAAGCTGACACCTGTGAACTAACTTAAACGCATGTTCTCTGACTCAG
7557	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TTCTGTTTTGGGCCAGGAACCGTTCTATAAATTGTTTTATTGACTACCG
7558	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	TAACACCGTCCAGAAATTTTGCCGTGTGTGCCCATACTTCTCTAGGGC
7559	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	AGAAGAAGGATCAGATGGAGAGTTGAAAACCTTTAGCTGGTAAGTACATGA
7560	literature	NA	NC_001345	9625578	Human herpesvirus 6, complete genome	1	CCGATACCGGCAAGATCTGTCGTCTGCAAACCTCGTTTTCCACCTTATGG
7561	literature	NA	NC_001664	9628290	Human herpesvirus 6, complete genome	1	CTGTGGTCCCTCCCTCATCTGTTATTCCCTTCCCTCTGCCACCGAT
7562	db mining	Hs.159568	AJ382620	4195401	qz04e10.x1 cDNA, 3' end /clone=IMAGE:2020554 /clone_end=3'	1	ACTACATTTTAATTAAGATTAAATGGGCATATTAGAAGTTTCTCAAAGTTAGGCT
7563	db mining	Hs.129055	NM_002540	4505490	Homo sapiens, Similar to outer dense fiber of sperm tails 2, clone MGC:9034 IMAGE:3874501, mRNA, complete cds /cds=(656,2947)	1	AAAAGGAGTGAGCTATCATCAGTGCTGTGAAATAAAGTCTGGTGTGCCA
7564	db mining	Hs.12329	AB014597	3327207	mRNA for KIAA0697 protein, partial cds /cds=(0,2906)	1	AAAGCCACCCTGTTCCAGTCAGCATATACAAGCTCTTAATATTCTGTT
7565	db mining	Hs.119177	NM_001659	4502202	ADP-ribosylation factor 3 (ARF3), mRNA /cds=(311,856)	1	AAATGTGGGATAACGCGATGACTGTGACCCTGGTTGGAAATTAACCTTGT
7566	db mining	Hs.12379	BC003378	13097227	Homo sapiens, ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R), clone MGC:5084 IMAGE:2901220, mRNA, complete cds /cds=(142,1122)	1	AACACAGAAACATTTGAGCATTTGATTTCTCGCATCCCTTCTCGTGAGCG
7567	db mining	Hs.319886	AL589290	13243062	DKFZp451F1715_r1 cDNA, 5' end /clone=DKFZp451F1715 /clone_end=5'	1	AACCTATCAAAGCCTAGCCTAAGGGCTGCCATCTCTGTCTAAATCTAGT
7568	db mining	Hs.315597	NM_015960	7705727	cDNA FLJ10280 fis, clone HEMBB1001288, highly similar to CGI-32 protein mRNA /cds=UNKNOWN	1	AACTGCATGGTATGAATTCAGAGTGTGACTTAAGGGTCAATTCAAAGCAG
7569	db mining	Hs.110457	AF071594	3249714	MMSET type I (WHSC1) mRNA, complete cds /cds=(29,1972)	1	ACAGACTTTGTAAATGTAGGAAATCTCTCCAAGTGGAAACGTGCTAACTT
7570	db mining	Hs.144904	NM_006311	5454137	nuclear receptor co-repressor 1 (NCOR1), mRNA /cds=(240,7562)	1	ACAGGCAATTCAGTGGACTATAATAATAGTGAGGGTTGAGATGTAGAGT
7571	db mining	Hs.118064	NM_022731	12232386	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(66,557)	1	ACAGGTCACAGTGGATTTCTTTTCAAACACTGACAATGTTTAGGTTTAAGC
7572	db mining	Hs.337616	NM_000753	4502924	phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA /cds=(0,3338)	1	ACCTCAAGCAGATGAGATTCAAGGTAA TTGAAGAGGCAGATGAAGAGGAAT
7573	db mining	Hs.152049	AW962287	8152099	EST374360 cDNA	1	ACCTTCTACACCACTGGAAAAATAACA TGGAGGTTTAGAGCCGTGCAAAAT
7574	db mining	Hs.115325	NM_003929	4506374	RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA /cds=(40,651)	1	ACTAAACTCTGAGGCCCTGAAGTTCTG TGATAGACCTTAAATAAGTGTCT
7575	db mining	Hs.119178	AK024466	10440445	mRNA for FLJ00059 protein, partial cds /cds=(2624,4057)	1	ACTGGGGTGGTGATGTTTTCTGTTCTG TTTTATTTTCTAACTCTGCTGAC
7576	db mining	Hs.183698	NM_000269	4557796	ribosomal protein L29 (RPL29), mRNA /cds=(29,508)	1	ACTTCATCATATAATTTGGAGGGAAGCT. CTGGAGCTGTGAGTCTCCCTGT
7577	db mining	Hs.15767	AB023168	4589541	mRNA for KIAA0949 protein, partial cds /cds=(0,2822)	1	AGAACGAGGAAGAGAACACAAGGAA TGATTCAAGATCCACCTTGAGAGGA
7578	db mining	Hs.108104	NM_003347	4507788	ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA /cds=(15,479)	1	AGAGAAATAGGCTTTCTAAGATGCTGC GATCCCGTTCTGCTGCCCGTAATA
7579	db mining	Hs.183593	NM_000980	11415025	ribosomal protein L18a (RPL18A), mRNA /cds=(19,549)	1	AGCACAAGCCACGCTTACCACCAA GAGGCCCAACACCTTCTTAGGTG
7580	db mining	Hs.121044	L39061	632997	transcription factor SL1 mRNA, partial cds /cds=(0,1670)	1	AGGCCAATCACTGCTGACTAAGAATT CATTATATTGGCTTAGTACACAGA
7581	db mining	Hs.309348	NM_032472	14277125	tc93c11.x1 cDNA, 3' end /clone=IMAGE:2073716 /clone_end=3'	1	AGGGAAGATTCTGTATACTTGTGG AGAGGAGGAATGTGTATAGTTACT
7582	db mining	Hs.16493	AK027866	14042851	cDNA FLJ14980 fis, clone PLACE4000192, weakly similar to ZINC FINGER PROTEIN 142 /cds=(114,3659)	1	AGTTTTAATACCTTAAGCTTTTCAAG ACCTAAGTGCAGCCGCTTTGGGA
7583	db mining	Hs.1342	NM_001862	4502982	cytochrome c oxidase subunit Vb (COX5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(21,410)	1	ATGTGCTGTAAAGTTTCTTCTTCCAG TAAAGACTAGCCATTGCATTGGC
7584	db mining	Hs.111076	NM_005918	5174540	malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(86,1102)	1	ATTGTGGGTGGCTCTGTGGGCGCAT CAATAAAAGCCGCTCCTGATTTTAT
7585	db mining	Hs.107476	NM_006476	5453560	ATP synthase, H+ transporting, mitochondrial F1F0, subunit g (ATP5JG), mRNA /cds=(73,384)	1	ATTTGAGTGTGTGTGGACCATGTGTG ATCAGACTGCTATCTGAATAAAAT

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7586	db mining	Hs.146354	NM_005809	5902725	peroxiredoxin 2 (PRDX2), mRNA /cds=(89,685)	1	CAAGCCCACCCAGCCGCACACAGGC CTAGAGGTAACCAATAAAGTATTAG
7587	db mining	Hs.12124	NM_018127	11875212	elaC (E. coli) homolog 2 (ELAC2), mRNA /cds=(0,2480)	1	CACCAGAGACAAGCAGAGTAACAGG ATCAGTGGGTCTAAGTGTCCGAGAC
7588	db mining	Hs.154023	AB011145	3043669	mRNA for KIAA0573 protein, partial cds /cds=(0,1356)	1	CAGGAGGTAGGGATCTGGCTGAGAG GGAATAATCTGAGCAAGGTATGAA
7589	db mining	Hs.109051	NM_031286	13775197	SH3BGL3-like protein (SH3BGL3), mRNA /cds=(71,352)	1	CAGTCCCTCTCCAGGAGGACCCCTA GAGGCAATTAAATGATGTCCTGTTT
7590	db mining	Hs.125307	AA836204	2910523	od22g11.s1 cDNA /clone=IMAGE:1368740	1	CATGAGAAGTATCTGCAATAACCCCA AGTCAACATTTAGGTTTGTGTACA
7591	db mining	Hs.16803	NM_018032	8922296	LUC7 (S. cerevisiae)-like (LUC7L), mRNA /cds=(71,1048)	1	CATGTTGAGTAGGAATAAATAAATCT GATGCTGCCCTCGTGGGCTGCGGG
7592	db mining	Hs.146580	NM_001975	5803010	enolase 2, (gamma, neuronal) (ENO2), mRNA /cds=(222,1528)	1	CCACCACCTCTGTGGCATTGAAATGA GCACCTCCATTAAAGTCTGAATCA
7593	db mining	Hs.14169	AK027567	14042333	cDNA FLJ14661 fis, clone NT2RP2002710, weakly similar to SH3-BINDING PROTEIN 3BP-1 /cds=(70,2481)	1	CCATGCCGCCTCGTTGGATTGTCGG AATGTAGACAGAAATGTACTGTTCT
7594	db mining	Hs.118625	NM_000188	4504390	hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein, mRNA /cds=(81,2834)	1	CCCACCGCTTTGTGAGCCGTGTCGTA TGACCTAGTAAACTTTGTACCAAT
7595	db mining	Hs.144505	NM_015653	13124762	DKFZP566F0546 protein (DKFZP566F0546), mRNA /cds=(377,1306)	1	CCCACGGGAGACTATTTACACAATT TAATACAGGAAGTCGATAATGAGG
7596	db mining	Hs.155751	NM_004889	4757811	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 (ATP5J2), mRNA /cds=(27,311)	1	CCCTCCGTGAGGAACACAATCTCAAT CGTTGCTGAATCCTTTCATATCCT
7597	db mining	Hs.10267	NM_015367	7662505	MIL1 protein (MIL1), nuclear gene encoding mitochondrial protein, mRNA /cds=(71,1231)	1	CCGTGTCTTCCAGCCCTAAAGGAAG GGCAGACCCGTGTCTTCCATGCC
7598	db mining	Hs.14632	BC008013	14124973	Homo sapiens, Similar to CG12113 gene product, clone IMAGE:3532726, mRNA, partial cds /cds=(0,2372)	1	CCTGAAGCACTTCACCTGGAATTGAT GTGTAGGCTTAAGGAGTATGTGAC
7599	db mining	Hs.125156	NM_001488	4503956	transcriptional adaptor 2 (ADA2, yeast homolog)-like (TADA2L), mRNA /cds=(0,1091)	1	CGCAGGCAAGAGCACTCATCAAGATA GATGTGAACAAACCCGGAAATC
7600	db mining	Hs.159545	NM_013308	7019400	platelet activating receptor homolog (H983), mRNA /cds=(219,1178)	1	CGCTCAAAGGTCACTGAGACTTTTGC CTCACCTAAAGAGACCAAGGCTCA
7601	db mining	Hs.152936	NM_004068	4757993	adaptor-related protein complex 2, mu 1 subunit (AP2M1), mRNA /cds=(135,1442)	1	CGGCCCTCAGTCCCTACTCTGCTTTGG GATAGTGTGAGCTTCATTTTGTAC
7602	db mining	Hs.110857	NM_016310	7708498	polymerase (RNA) III (DNA directed) polypeptide K (12.3 kDa) (POLR3K), mRNA /cds=(39,365)	1	CTAGTGTGTGCTTGCCTTGTCCCTCG GGGTAGATGCTTAGCTGGCAGTAT
7603	db mining	Hs.118666	NM_025207	13376805	hypothetical protein PP591 (PP591), mRNA /cds=(820,1704)	1	CTTTCAGATTCCTCTGGTCTCCGTC CGAAACGCTACCTCTTCCAGGC
7604	db mining	Hs.16390	AK024453	10440419	mRNA for FLJ00045 protein, partial cds /cds=(106,924)	1	GAAATTTACAGGCCAGGCGACATCTT TTATTTATTTCAATTATGTTGGCCA
7605	db mining	Hs.109302	AA808018	2877424	nv64d09.s1 cDNA, 3' end /clone=IMAGE:1234577 /clone_end=3'	1	GACTCCCTCAACACCCCAAACTCTA AATGCCACGGTCATCTGTTTCTAT
7606	db mining	Hs.111126	NM_004339	11038670	pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA /cds=(210,752)	1	GAGCAGCCACAAAACCTGTAACCTCAA GGAAACCATAAAGCTTGGAGTGCC
7607	db mining	Hs.127376	NM_021645	11063982	KIAA0266 gene product (KIAA0266), mRNA /cds=(733,3033)	1	GCAGCAACAGAGGGTCACTGACAG GATGTTCTGACACACCAATGTAACT
7608	db mining	Hs.108196	NM_016095	7708366	HSPC037 protein (LOC51659), mRNA /cds=(78,635)	1	GCCAAACATGCTGACCGGTGCTTATC CTCTAAGCCCTGATCCACAATAAA
7609	db mining	Hs.117487	AF040965	2792365	unknown protein IT12 mRNA, partial cds /cds=(0,2622)	1	GCCAGTGTAATTTCTGTCAACCCAGG ACGTTTGCCTTCATGTGTAGAATT
7610	db mining	Hs.107882	NM_018171	8922576	hypothetical protein FLJ10659 (FLJ10659), mRNA /cds=(38,1000)	1	GCCCCAGCACTAGTAGAGATGCGCG ATACAGGTCTAGTTTCGGTAAGTGT
7611	db mining	Hs.147585	NM_024785	13376147	hypothetical protein FLJ22746 (FLJ22746), mRNA /cds=(266,1072)	1	GGCCAGATTTTGACTCCAGATTCCT TTACAAAACGCACCTCATTCATTCA
7612	db mining	Hs.153357	NM_001084	4505890	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 (PLOD3), mRNA /cds=(216,2432)	1	GGGACTCCCCCGCGTGAATAAATTATTA ATGTTCCGCAGTCTCACTCTGAAT
7613	db mining	Hs.148495	NM_002810	5292160	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4), mRNA /cds=(62,1195)	1	GGGACTGCATGGGAAGCACGGAATA TAGGGTTAGATGTGTATTCTGTA
7614	db mining	Hs.13144	NM_014182	7661819	HSPC160 protein (HSPC160), mRNA /cds=(53,514)	1	GGGGTTCGTGTCTTTGGCATCAACAA ATACTGAGGGATGGGTTTGGGAC
7615	db mining	Hs.1189	NM_001949	12669913	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(66,1463)	1	GGGTGACCTGTTCTCTAGCTGTGATC TTACCACTTCAAAATGGGTGTAATT
7616	db mining	Hs.12284	BC001699	12804564	Homo sapiens, clone IMAGE:2989556, mRNA, partial cds /cds=(0,370)	1	GGTGTGAACGGGCTGACTTGGTGAA TTGGGCAACTCCTTATAGTGTGTG

Table 8

7617	db mining	Hs.158380	AI381581	4194382	td05e04.x1 cDNA, 3' end /clone=IMAGE:2074782 /clone_end=3'	1	GTACCACTTGAATGATTTTCAGTCAATT TTGAACCCCTTTGGAAAGAGGTG
7618	db mining	Hs.1390	BC000268	12653014	Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 2, clone MGC:1664 IMAGE:3352313, mRNA, complete cds /cds=(58,663)	1	GTGAAACCCCGTCTCTGCTAAAAATA CAAAAATTAGCTGGCGCTGGTGGC
7619	db mining	Hs.115808	NM_002287	11231175	leukocyte-associated Ig-like receptor 1 (LAIR1), transcript variant a, mRNA /cds=(57,920)	1	GTTCTCTGGGTTGTGCTTTACTCCAC GCATCAATAAAATATTTGAAGGC
7620	db mining	Hs.119960	AL117477	5911950	mRNA; cDNA DKFZp727G051 (from clone DKFZp727G051); partial cds /cds=(0,1423)	1	TACTGCCAACTGACCTTATAACCCCTC TGCACCTTCAAAAAGATTCATGGT
7621	db mining	Hs.154073	NM_005827	5032212	UDP-galactose transporter related (UGTREL1), mRNA /cds=(87,1055)	1	TCAAACAGTGACATCTCTTGGGAAAA TGGACTTAATAGGAATATGGGACT
7622	db mining	Hs.11747	NM_017798	8923363	hypothetical protein FLJ20391 (FLJ20391), mRNA /cds=(9,602)	1	TCACCTCCTCGAACTGTTACTGCCT GAATGGAGTCCTGGACGACATTGG
7623	db mining	Hs.10881	AB011113	3043605	mRNA for KIAA0541 protein, partial cds /cds=(0,3484)	1	TCCACTTAATAGACTCTATGTGTGCT GAATGTTCTGTGTACATATGTGT
7624	db mining	Hs.153850	AK024476	10440465	mRNA for FLJ00069 protein, partial cds /cds=(2657,4396)	1	TCCCGCAGAGTGACAGACAGGAAG CTGGAGATGCTTTTATAAGTCACA
7625	db mining	Hs.247870	AL035694	4678462	DNA sequence from clone 33L1 on chromosome 6q14.1-15. Contains the gene for novel T-box (Brachyury) family protein. Contains ESTs, STSs, GSSs and two putative CpG islands /cds=(0,1505)	1	TCTAGGACCTTAGGAAGCTTAACCTC GTCATCATCTCAAGTATCTGCACA
7626	db mining	Hs.324648	NM_003128	4507194	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN /cds=UNKNOWN	1	TCTTCGCCATCTCCTCTGATAAACA CGAGGTGTCTGCCAGCACCCAGAG
7627	db mining	Hs.118722	NM_004480	4758407	fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA /cds=(718,2443)	1	TGATATGTTGATCAGCCTTATGTGGA AGAACTGTGATAAAAAGAGGAGCT
7628	db mining	NA	AL134726	6602913	DKFZp547A1290_r1 cDNA, 5' end /clone=DKFZp547A1290 /clone_end=5'	1	TGCAGTATTTTCAAACCTTCTGGTCG CAAACCCATTAGTAGTTTGTGAAA
7629	db mining	Hs.166887	NM_003915	4503012	copine I (CPNE1), mRNA /cds=(156,1769)	1	TGCTGCTCTTGATCCACCTTTGCTC CTGACAACCCCTCATTAATAAAGA
7630	db mining	Hs.146324	AK023182	10434993	cDNA FLJ13120 fis, clone NT2RP3002682, highly similar to CGI-145 protein mRNA /cds=(176,961)	1	TGGTTTGTTCATGGATGTTACTAAG AGCTGAGAACAGGGCTGGACACA
7631	db mining	Hs.12436	AK026309	10439130	cDNA: FLJ22656 fis, clone HSI07655 /cds=UNKNOWN	1	TGTTCTGAATGTTGGTAGACCCTTCA TAGCTTTGTTACAATGAACCTTG
7632	db mining	Hs.15164	NM_006333	5453582	nuclear DNA-binding protein (C1D), mRNA /cds=(117,542)	1	TGTTGATGGATGAATTTTGGCATGAT GACTGTACTCTCAATAAAGGCTGA
7633	db mining	Hs.130743	AA642459	2587677	ns30d01.s1 cDNA, 3' end /clone=IMAGE:1185121 /clone_end=3'	1	TTCATCCTGTGAGTGCTGGGGAGGA GGAGTAGATACAGACTGAGTGAGAG
7634	db mining	Hs.16492	NM_015497	13794264	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(42,1709)	1	TTCAATTTCTCGGGAAGTCAAGGTTA CATCTTGACAGAGGTGTTTGTGAGA
7635	db mining	Hs.122552	NM_016428	7705291	G-2 and S-phase expressed 1 (GTSE1), mRNA /cds=(70,2232)	1	TTCTAAGCCGAACCAATCCTTTGCC TTGAAAGAACGCCCTAAAGTGGT
7636	db mining	Hs.312510	AI174807	6361196	HA2528 cDNA	1	TTTGTGTTGTTGTTTCAGATAGGGTCT CCCTCTGTCACCCAGGCTGCAGT
7637	db mining	Hs.108258	NM_012090	10048480	actin cross-linking factor (ACF7), transcript variant 1, mRNA /cds=(51,18343)	1	TTTTGTAATCACGGACACCTCAATTA GCAAGAACTGAGGGGAGGCTTT
7638	db mining	Hs.111092	NM_024724	13376033	hypothetical protein FLJ22332 (FLJ22332), mRNA /cds=(275,1255)	1	CGGTGTGGAAAATGTTGCTCTTTGAG TGGCAAGAAATTAGAAAAATCTTCA
7639	db mining	Hs.114311	NM_003504	4502712	CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like (CDC45L), mRNA /cds=(24,1724)	1	CTGAAAGCTGAGGATCGGAGCAAGT TTCTGGACGCCTTATTTCCCTCCT
7640	db mining	Hs.11081	NM_025241	13376853	UBX domain-containing gene 1 (UBXD1), mRNA /cds=(96,1421)	1	GTTGGCCTCAGCCCTGTGGGTCTGT CTCATGCTCTCCCTGTTCTCTCCC
7641	db mining	Hs.100217	NM_005892	5174400	formin-like (FMNL), mRNA /cds=(39,1430)	1	TAGCCATACTTAGCCTCAGCAGGAGC CTGGCCTGTAACCTTAAGGTGCA
7642	db mining	Hs.12258	AL137728	6808258	mRNA; cDNA DKFZp434B0920 (from clone DKFZp434B0920) /cds=UNKNOWN	1	TGAGGGCTGTGTGACCTTTGAGAG GATTTGAAATTGCTTCATATTGTGA
7643	db mining	Hs.155462	NM_005915	7427518	minichromosome maintenance deficient (mis5, S. pombe) 6 (MCM6), mRNA /cds=(61,2528)	1	TGTGTAAGAAAAGGCCCACTACTTTT AAGGTATGTGCTGTCTATTGAGC
7644	db mining	Hs.165998	NM_015640	7661625	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(85,1248)	1	TTGTTGGTAGGCACATCGTGTCAAGT GAAGTAGTTTTATAGGTATGGGTT
7645	db mining	Hs.164207	NM_024805	13376184	hypothetical protein FLJ21172 (FLJ21172), mRNA /cds=(138,1169)	1	TTTCTAGCTTTTCCGTGTATCTAAACA CAATTTGCTACACAAGTCACTGT
7646	db mining	Hs.150275	D87682	1683699	mRNA for KIAA0241 gene, partial cds /cds=(0,1568)	1	ACTGTGGCAGATGTTTGTATCAGAAA GGTAGTCTCTTTGCTCTGGTAGT

Table 8

7647	db mining	Hs.11039	NM_024102	13129109	hypothetical protein MGC2722 (MGC2722), mRNA /cds=(69,1097)	1	CATCTTCTGCCCTGGTCCCCTTTCTC
7648	db mining	Hs.102708	NM_015398	7661561	DKFZP434A043 protein (DKFZP434A043), mRNA /cds=(697,1425)	1	TTGATGTGGAAAGTCTGAATGCAG
7649	db mining	Hs.109646	NM_002493	4505364	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) (NDUFB6), mRNA /cds=(68,454)	1	CGCTCTAATACTGCATTCTGTTTCTC
7650	db mining	Hs.142307	AL137273	6807710	mRNA; cDNA DKFZP434I0714 (from clone DKFZP434I0714) /cds=(0,412)	1	CTTTTGTGCCCTGATTGTAATCCA
7651	db mining	Hs.16297	NM_005694	5031644	COX17 (yeast) homolog, cytochrome c oxidase assembly protein (COX17), mRNA /cds=(86,277)	1	CTGGAGACTGGAGAAGTAATCCACC
7652	db mining	Hs.11184	NM_017811	8923387	hypothetical protein FLJ20419 (FLJ20419), mRNA /cds=(191,907)	1	AATGAAAGAAATTCCTGATCAACA
7653	db mining	Hs.12013	NM_002940	4505558	ATP-binding cassette, sub-family E (OABP), member 1 (ABCE1), mRNA /cds=(117,1916)	1	TCAGTGTTTCGTTATTCCATATCAGTG
7654	db mining	Hs.155485	NM_005339	12545382	huntingtin interacting protein 2 (HIP2), mRNA /cds=(77,679)	1	GCTTTTACTGTCAAAGATTGTGT
7655	db mining	Hs.154573	AW955094	8144777	EST387164 cDNA	1	TGCATGAGAGCCCTAGGATTTAAAT
7656	db mining	Hs.142157	AF080255	5733121	Iodestar protein mRNA, complete cds /cds=(30,3518)	1	ATGAAATGGTGGTCTGCTGTGTGA
7657	db mining	Hs.1191	AK025879	10438273	cDNA: FLJ22026 fls, clone HEP08537 /cds=UNKNOWN	1	TGTGCTAAGCCTGATGAAATGTGCTC
7658	db mining	Hs.13340	NM_003842	4504340	histone acetyltransferase 1 (HAT1), mRNA /cds=(36,1295)	1	CTTCAATCTCCATGAACCATCGT
7659	db mining	Hs.108110	NM_014034	7661591	DKFZP547E2110 protein (DKFZP547E2110), mRNA /cds=(192,806)	1	AAATGATCTCCCTTTATTACCTCCCA
7660	db mining	Hs.123295	AA833793	2908561	cd81g07.s1 cDNA /clone=IMAGE:1372476	1	AAGGTTACCAGCGTTTGAATTTA
7661	db mining	Hs.126565	AB020668	4240210	mRNA for KIAA0861 protein, partial cds /cds=(0,2948)	1	ACACACTAATGTAAACCATTTTGAAG
7662	db mining	Hs.155174	AB007892	2887434	KIAA0432 mRNA, complete cds /cds=(0,2251)	1	GTTGAAGTGGATTATGCAGGCA
7663	db mining	Hs.116445	AA648776	2575205	ns24d11.s1 cDNA, 3' end /clone=IMAGE:1184565 /clone_end=3'	1	ATCAGGAGAAATGTCAAAGAAGTCCTT
7664	db mining	Hs.124933	AA825303	2898605	oc67e04.s1 cDNA, 3' end /clone=IMAGE:1354782 /clone_end=3'	1	TATGTGGATTGCCCGAGCTTCTCT
7665	db mining	Hs.313267	AW295641	6702277	UI-H-BW0-aipe-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729975 /clone_end=3'	1	ATTGTGCCACTGTTTCCAGCCTGGG
7666	db mining	Hs.313203	AW293882	6700518	UI-H-BW0-ain-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729941 /clone_end=3'	1	CAATACAGTGAGACCCTGTCTCAA
7667	db mining	Hs.105488	AA521017	2261560	aa70f05.s1 cDNA, 3' end /clone=IMAGE:826305 /clone_end=3'	1	CGTCAAAGTCAATCCCAAAACAGATA
7668	db mining	Hs.125802	AA806833	2876409	oc29b10.s1 cDNA, 3' end /clone=IMAGE:1351099 /clone_end=3'	1	AGCCCTATGAGGATGTGAGCATCA
7669	db mining	Hs.313274	AW295745	6702381	UI-H-BW0-aiw-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730834 /clone_end=3'	1	ACGACTTGCTCAAGAGTAAAGATTAT
7670	db mining	Hs.320376	BF512113	11597325	UI-H-BW1-ami-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070302 /clone_end=3'	1	ACTGCTCTGTACAGGAAGCTTGCA
7671	db mining	Hs.315341	BE675056	10035597	7f01f10.x1 cDNA, 3' end /clone=IMAGE:3293419 /clone_end=3'	1	TGTTGAGGAAAGGAAGGGCATTTG
7672	db mining	Hs.320407	BF512394	11597660	UI-H-BW1-amc-f-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069456 /clone_end=3'	1	TCTAACATGGATTCTGAGTTGTA
7673	db mining	Hs.313347	AW297156	6703802	UI-H-BW0-ajd-b-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731329 /clone_end=3'	1	GTGGATGAGTAGGGAGTGGCGGAGA
7674	db mining	Hs.123298	AA809468	2878874	ob85a10.s1 cDNA, 3' end /clone=IMAGE:1338138 /clone_end=3'	1	CAGGGACGAGATGAGCAGGTCAGG
7675	db mining	Hs.320416	BF512570	11597749	UI-H-BW1-amf-e-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069791 /clone_end=3'	1	GGTGTTCGTGTTAGTGCCAAGATTGC
7676	db mining	Hs.309262	AI440532	4300887	CM4-NT0290-150101-684-e05 cDNA	1	TTCGTTGTAGAGAGAGTTCGTTCC
7677	db mining	Hs.313338	AW297010	6703646	UI-H-BW0-ajf-d-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731441 /clone_end=3'	1	ACTAGAGTCCAGGTAATAGTAGTGA

Table 8

7678	db mining	Hs.315325	BE646400	9970711	7e86c01.x1 cDNA, 3' end /clone=IMAGE:3292032 /clone_end=3'	1	CCCTCCCTATCTTTTATGGGTAATTT GATTATACACGGTGCTTGAATGT
7679	db mining	Hs.313172	AW293016	6699652	UI-H-BW0-aih-f-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729239 /clone_end=3'	1	TATGTCTTCTTACCCACGACCCCTA ATTTAAATACAGATCCCTGAGGT
7680	db mining	Hs.313351	AW297413	6704049	UI-H-BW0-ais-b-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730208 /clone_end=3'	1	AAAACCTTGACAGTTCATTTCACCAA GCACCTATCAGGTATTTGGCAGGT
7681	db mining	Hs.313365	AW297482	6704118	UI-H-BW0-aja-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730920 /clone_end=3'	1	AGTGCCCATGCTGTTTCAGATGCTCT TCTAGCTCCTGGAGATACATCAGT
7682	db mining	Hs.313358	AW297377	6704013	UI-H-BW0-aij-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730381 /clone_end=3'	1	TGAGCTTCTGCTAGTAATTCCTTCAG GGGATTTCCTCCATGGCCGTAAGT
7683	db mining	Hs.320474	BF513180	11598359	UI-H-BW1-amf-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070115 /clone_end=3'	1	GAGGGTGTCTGCTAATGATTTCCGAA AAGTTCTTCAAACACTCCGAAGT
7684	db mining	Hs.313382	AW297707	6704343	UI-H-BW0-ajh-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731915 /clone_end=3'	1	ACCAGTGTGATGAGTTTTGACAAGAG ACAAAAGGAAAGGGTGGGAGAAGT
7685	db mining	Hs.125779	AA810831	2880442	oa76d09.s1 cDNA, 3' end /clone=IMAGE:1318193 /clone_end=3'	1	GCTGGTTGTTGCCCTTCAAGACAGCC AACTACCATTATTCAACAGAAGT
7686	db mining	Hs.313389	AW297882	6704507	UI-H-BW0-aju-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733036 /clone_end=3'	1	AGTCTGTCTATTCTCTCTCTTTAGCT CTGTCTGTTGCTCAAAATCAAGT
7687	db mining	Hs.313391	AW297905	6704541	UI-H-BW0-aju-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2733188 /clone_end=3'	1	GCCAAAGGTGAGTCAAAACACTGCTCT TCAGAAAGCAATTATTTGAAAAGT
7688	db mining	Hs.309446	AI492055	4393058	tg12a01.x1 cDNA, 3' end /clone=IMAGE:2108520 /clone_end=3'	1	CATTGTCCCTCCCGCTGTGCTCTCAG GCAATAAATGATTGTATTCT
7689	db mining	Hs.313311	AW296433	6703069	UI-H-BW0-aiq-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730128 /clone_end=3'	1	GGTCAGAAACAGGCCACAGAGACT CTGGAGGGTCTTCTCTTGTGTTCT
7690	db mining	Hs.319887	BF507608	11590906	UI-H-BW1-ana-e-05-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071720 /clone_end=3'	1	TTCAACTGCTTTGGCACTGCCATGGG TACCTGAGGATAAGAGAGATGTCT
7691	db mining	Hs.255237	AW293790	6700426	UI-H-BI2-ahp-e-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2727635 /clone_end=3'	1	GGGTTGACTAAATGCACATGGGCTTA TCTTTACCTCTCCAGAAATGTCT
7692	db mining	Hs.313363	AW297459	6704095	UI-H-BW0-ais-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730436 /clone_end=3'	1	TGCATGACCAGAAACACTGCCTGATA CAGTAAGCAGAGGTAGCTGTCTCT
7693	db mining	Hs.320367	BF512169	11597272	UI-H-BW1-ami-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070074 /clone_end=3'	1	ACCTGCCAGCCAGCCCAACTATAA ACTGTGTGACACCCAAATTTATCT
7694	db mining	Hs.320440	BF512733	11597912	UI-H-BW1-amm-d-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070494 /clone_end=3'	1	GGTTTCTGAGGTGATTCTAATATGCA GTCATGGTTAAGAACCTGTGATCT
7695	db mining	Hs.313374	AW297607	6704243	UI-H-BW0-ajg-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731854 /clone_end=3'	1	AAGCCTTGGACCACTTCCCGTTTCT CTCTTGCTCCTGCCAAAAGATCT
7696	db mining	Hs.313355	AW297325	6703961	UI-H-BW0-aij-a-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730135 /clone_end=3'	1	ACCCAAAGGATGGTGTCTCCTGTCCC AGTTGAAAAGGTTTCTACCTAGCT
7697	db mining	Hs.320420	BF512599	11597778	UI-H-BW1-amf-h-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069925 /clone_end=3'	1	TGGTTGAATACGCAGGAACACCCACA GTACCCAGGGACTAATAAATAGCT
7698	db mining	Hs.118899	AA243283	1874128	zs13g11.s1 cDNA, 3' end /clone=IMAGE:685124 /clone_end=3'	1	TTAGGGCAGTGGAGAATCAGGGTGT ATCTAATAAATTCCTTCATGGAGCT
7699	db mining	Hs.105228	AA489212	2218814	aa57d11.s1 cDNA, 3' end /clone=IMAGE:825045 /clone_end=3'	1	GCAGATGTCTGCGTCATGGTTTATTA CTCCTGTGTTTCGTTCAAGGAGCT
7700	db mining	Hs.297505	BF514865	11600044	UI-H-BW1-anf-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082534 /clone_end=3'	1	TGTCTGATTGAGTCCAGTAGTAC ACTGAAAATAATCCCGTAAAAGCT
7701	db mining	Hs.320492	BF513340	11598519	UI-H-BW1-amk-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070050 /clone_end=3'	1	CTCCCTTCCACCATACACACTCC CAGCTCATTTTGATTCCTTTCTCT
7702	db mining	Hs.304837	AW292802	6699438	UI-H-BW0-ajf-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729615 /clone_end=3'	1	GGTGAAATTGACTGGGTTCTCTCCT ACCTCTCTTCCGTAGCAATTCCT
7703	db mining	Hs.24656	BF507762	11591060	KIAA0907 protein (KIAA0907), mRNA /cds=(26,1720)	1	ACTAATTCCTGCTGTGCGCCCTGAAC ATGAAGATATAATGGACGATCCCT
7704	db mining	Hs.320460	BF512975	11598154	UI-H-BW1-amh-b-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069659 /clone_end=3'	1	TTAAAGGCTCAAACCTACCTCAGACA CTGCTCTACCCATCCCATCCCT
7705	db mining	Hs.313384	AW297745	6704381	UI-H-BW0-aiy-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730954 /clone_end=3'	1	CCCTTTGTGAGAAGAAGCAGGTTTCC TTCTCTATGGAATTGATGTGACCT

Table 8

7706	db mining	Hs.105105	AA419402	2079198	zu99a12.s1 cDNA, 3' end /clone=IMAGE:746110 /clone_end=3'	1	TTCTACCCATCACACAGATTCTTCCA CTTAATAAAATCCATCACCTACCT
7707	db mining	Hs.123180	AA805419	2874169	oc13g03.s1 cDNA, 3' end /clone=IMAGE:1340788 /clone_end=3'	1	TCATTACTGTTGTGAAGGCTCTTCAA GAGAGAAAGATGAAGCTGAAACCT
7708	db mining	Hs.297396	BF515183	11600450	UI-H-BW1-ani-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082728 /clone_end=3'	1	GCTGTCCGTGAAGCACTCTCAAGTC AGGAACTGAACTAAGAACTTTACT
7709	db mining	Hs.334992	AI084211	3422634	RST20881 cDNA	1	CTCCTGTAATCCCAGCACTGGAGCTT GCAGTGAGCCAAGATCATGCCACT
7710	db mining	Hs.313273	AW295743	6702379	UI-H-BW0-ahw-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730830 /clone_end=3'	1	TTGGTCACCAACACCTGGGTGCTGAA TGCTTTGCTCTCTAAAGGTAAC
7711	db mining	Hs.319891	BF507631	11590929	UI-H-BW1-ana-h-01-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071856 /clone_end=3'	1	GCAACAATTCTTTGAAAGTGACTCT CTAGGGTCCGGAGAATGGTGTGAT
7712	db mining	Hs.320422	BF512614	11597793	UI-H-BW1-amg-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069622 /clone_end=3'	1	TCATCTCTGTAGGCTTCTCTAATCCTA TGCGGAGCCAAATATAGACGGAT
7713	db mining	Hs.319872	BF507414	11590721	UI-H-BW1-amz-a-11-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071517 /clone_end=3'	1	CTTTGTATTTCAAAGAAAGTAGCCCC TTGGCTCTGATATTAGTTGCAGAT
7714	db mining	Hs.264120	AI523641	4437776	601436078F1 cDNA, 5' end /clone=IMAGE:3921187 /clone_end=5'	1	TTTAGGAGCTGACCATACATGATGAG TGATACAGCCTGTACTTTGCTCAT
7715	db mining	Hs.105284	AA491263	2220436	aa49d04.s1 cDNA, 3' end /clone=IMAGE:824283 /clone_end=3'	1	ACTGGGATGAGATGAGATTCAAGGCA CTTTTGAGGGGTGAGCTAGCCAT
7716	db mining	Hs.124376	AA831043	2904142	oc58h02.s1 cDNA, 3' end /clone=IMAGE:1353939 /clone_end=3'	1	AGGCTGTTGCTGCACGGGCTTTTCAA AAGCGACTCATTATGAAGAAGTAAT
7717	db mining	Hs.309144	AI384035	4196816	td05c02.x1 cDNA, 3' end /clone=IMAGE:2074754 /clone_end=3'	1	GCACTCCAGCCTGGGCAACAAGAGC GAAACTCTGCCTCCATAAATAAAT
7718	db mining	Hs.301325	BF514004	11599183	UI-H-BW1-amv-e-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071311 /clone_end=3'	1	CGGGCGGTGGCGGCTGCCTGGGAG AAGATGAATCTTTCATGAGTATTTG
7719	db mining	Hs.319904	BF507742	11591040	UI-H-BW1-anc-f-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3072122 /clone_end=3'	1	GATGGAACCTCAAGGTGCTTTACGCTT TCCTCAGTCTTACCAGGAGGCTTG
7720	db mining	Hs.320092	AI392740	4222287	tg23f02.x1 cDNA, 3' end /clone=IMAGE:2109627 /clone_end=3'	1	ACCAACCCCTATGGACAACCTTGATCTT GAACCTCTAGCTTTCAGACCTGTG
7721	db mining	Hs.313371	AW297578	6704214	UI-H-BW0-ajg-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731708 /clone_end=3'	1	AATGTAGCTGACATTGGAGCCACCGC CCATAGAAGAAGGCTAAAACCTGTG
7722	db mining	Hs.320444	BF512784	11597963	UI-H-BW1-amm-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070698 /clone_end=3'	1	CTTCACTGACGATCTGAGACACTAGG CAGGTTGGAAAGGGTGGAGTGGTG
7723	db mining	Hs.320473	BF513155	11598334	UI-H-BW1-amj-b-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070013 /clone_end=3'	1	GCCCCCTGGTGGTTGGAAAAGTGTTCT GAATCCAATAAAAGGAAAGCGGTG
7724	db mining	Hs.320419	BF512597	11597776	UI-H-BW1-amf-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069921 /clone_end=3'	1	CAACAGTGGCAAGAGTAGCCAGCCC ATAGGACGGAATGAAATCAAGGTG
7725	db mining	Hs.320365	BF512157	11597260	UI-H-BW1-ami-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070026 /clone_end=3'	1	CATCCTTAGATGCCAGTCTTCACTTT GGGTATTTTCTGCCCTCCTCAGTG
7726	db mining	Hs.299471	BF513893	11599072	UI-H-BW1-amq-d-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070874 /clone_end=3'	1	ACCAACAGTACCGTTATTGCCACCAC AAGTAAACCACTCCCTCACTTCTG
7727	db mining	Hs.313368	AW297544	6704180	UI-H-BW0-aja-g-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731200 /clone_end=3'	1	AGGCTAAATCAGAGCTTTCCTCCCCA GATAAAGGAAATTTTCCCTCCCTG
7728	db mining	Hs.105170	AA481410	2210962	zv02g12.s1 cDNA, 3' end /clone=IMAGE:746374 /clone_end=3'	1	AACCTCCAGAGGCAGGAGATTAGACA GGGATGACAGTTAAGGGGTACTG
7729	db mining	Hs.313251	AW295130	6701766	UI-H-BW0-ait-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730495 /clone_end=3'	1	ACCTCTCGTTGTATTTACCTTTTAC TTACAAACAAGCTCATGCCACTG
7730	db mining	Hs.297392	BF514201	11599380	UI-H-BW1-ani-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082401 /clone_end=3'	1	GATCAAAACAAGGTCCTTGACTTTTT GCAGGGGCAGCCTGGCAATCAATG
7731	db mining	Hs.122417	AA761212	2810142	nz20c03.s1 cDNA, 3' end /clone=IMAGE:1288324 /clone_end=3'	1	CCTAAATGTTGTCCCTCAGAGATGCA CAGATGTATATGGGTAAGGAAATG
7732	db mining	Hs.297469	BF512785	11597964	UI-H-BW1-amm-h-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070700 /clone_end=3'	1	CCAACCATAGTCATGAAGCTGCTTCT GTTCCCAATGCAATCCCATTTGTTG
7733	db mining	Hs.313275	AW295750	6702366	UI-H-BW0-ahw-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730868 /clone_end=3'	1	GCTTTTCAATGCTTCCGAAACTGAGT GCTAACAGGGGCAATTAGTGCTGG

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7734	db mining	Hs.313173	AW293031	6699667	UI-H-BW0-aih-g-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729299 /clone_end=3'	1	AGTTCCTGTAACAGTTAAACTTTCTT GCCAGCTCTCAGGTTATCACTGG
7735	db mining	Hs.320386	BF512295	11597474	UI-H-BW1-amb-e-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069388 /clone_end=3'	1	GTGTGTAATGAGTGTGAGATCTTTT CTTGAAAACAGGTTTGGATTGGGG
7736	db mining	Hs.320429	BF512664	11597843	UI-H-BW1-amb-f-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069844 /clone_end=3'	1	AGGGTCCACAAGGAGAATATTTTCTT AAAGTAACCTCCGTGATTGCGGGG
7737	db mining	Hs.123352	AA811133	2880744	oa98b10.s1 cDNA, 3' end /clone=IMAGE:1320283 /clone_end=3'	1	GCTCCCTATGCCTGTGTAGCAGAAT CTAAGATAATCATGTGAACGGG
7738	db mining	Hs.320389	BF512323	11597502	UI-H-BW1-amb-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069497 /clone_end=3'	1	TTGCTCTGTTTCTTTTATCTCCCTAT GTTTCATCTTAGTGACGGCAGGG
7739	db mining	Hs.120563	AA741116	2779708	nz04f08.s1 cDNA, 3' end /clone=IMAGE:1286823 /clone_end=3'	1	ACAGTTGCCTTTGAGATTCTGTATTT CTGCATGAATAAATCCATAAGGG
7740	db mining	Hs.320373	BF512098	11597310	UI-H-BW1-ami-f-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070222 /clone_end=3'	1	GTCCTTGGAAGGTAACACTTGTGATT GGAACCACTCTCAAGCTGAACGG
7741	db mining	Hs.320490	BF513327	11598506	UI-H-BW1-amk-a-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069998 /clone_end=3'	1	ATTCAATTCATTCAATCAACAAGCACTT AAAACAATGCCTGTGTGCCAGG
7742	db mining	Hs.313290	AW296074	6702710	UI-H-BW0-aii-h-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730852 /clone_end=3'	1	CACACCCAGCCCCATTCAAAAGGAC TATAAATCTACACCCAGTCACG
7743	db mining	Hs.320390	BF512330	11597509	UI-H-BW1-amb-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069537 /clone_end=3'	1	GGCATAGTAGTGCTAAACAGAGGTG GAAGTAGGAAGGGAGTTTGAACG
7744	db mining	Hs.297397	BF507606	11590904	UI-H-BW1-ana-e-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071714 /clone_end=3'	1	CTAGTCTGCCCCACCTCCCAAGT ATTACCCCTCCTAAGTCTGCTAG
7745	db mining	Hs.309256	AI373161	4153027	qz13a01.x1 cDNA, 3' end /clone=IMAGE:2021352 /clone_end=3'	1	AGATAAGCAGGATAAACAAGACAGGT TGGATTGTGATCAGCTCTATGGAG
7746	db mining	Hs.343303	BF513322	11598501	UI-H-BW1-amk-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069986 /clone_end=3'	1	GATGGCTAGGACAAGATGATTACAA GAGCGTGGCGGGAGGGACGGCGAG
7747	db mining	Hs.301870	BF507614	11590912	UI-H-BW1-ana-f-03-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071764 /clone_end=3'	1	CCGTGTCTGGATTGTGTGCTTACTT CTAAGGTGCACATACTTCATAAG
7748	db mining	Hs.300479	AW452510	6993286	UI-H-BW1-ame-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069598 /clone_end=3'	1	GTATCTCTGCACCTCACTACTACCT TCACCTCTGGAGACCTGGGCAAG
7749	db mining	Hs.320387	BF512301	11597480	UI-H-BW1-amb-e-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069401 /clone_end=3'	1	AACACACCACCAACATTCTTCCCAT CCTTCTTACCAACACGCTACAAG
7750	db mining	Hs.122854	AA292626	1940611	zs57h08.r1 cDNA, 5' end /clone=IMAGE:701631 /clone_end=5'	1	ACAATTGGAGTTGGGGCTGTCAACCA CTAAGTGTGTCAACCACAGAAAG
7751	db mining	Hs.300488	AW453029	6993805	UI-H-BW1-ama-c-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069308 /clone_end=3'	1	TTAGGGCAAAAGTCTAGTGGCGGC AGCTTCTTGTGTAGAGCTGGTTTC
7752	db mining	Hs.335081	AI380942	4190807	tg18c08.x1 cDNA, 3' end /clone=IMAGE:2109134 /clone_end=3'	1	AGTGATGCTTGCCTTTTCGCTTTCCCT AAAGATGTCAATTGAAAACAGTC
7753	db mining	Hs.313822	AW452916	6993692	UI-H-BW1-amd-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069267 /clone_end=3'	1	CCCAGCTTCATTAATGTGAATGGTGG CAGACACCTCTAGCTATAGAGCTC
7754	db mining	Hs.309486	AI523959	4438094	tg98f09.x1 cDNA, 3' end /clone=IMAGE:2116841 /clone_end=3'	1	GAGCCAAGATTGGGCCACTGCACCTC CAGCCTGGGTGACAGAGTGAGACTC
7755	db mining	Hs.303928	AI084223	3422646	oy72g05.x1 cDNA, 3' end /clone=IMAGE:1671416 /clone_end=3'	1	GAGCCGAGATTGCATCACTGCACCTCC AGCCTGGTCAACAGACGAGACTC
7756	db mining	Hs.313170	AW292942	6699578	UI-H-BW0-alg-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729252 /clone_end=3'	1	TTCAAGTCATGCAGCAACATCCGCTTA ATGCCTCCTAAGTGCAGAACTCTC
7757	db mining	Hs.313795	AW452553	6993329	UI-H-BW1-ame-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069788 /clone_end=3'	1	GGTCCTCTTCTCTACTCTCCCTAG TAACTAACCACCAAGGCTAAATC
7758	db mining	Hs.319883	BF507567	11590865	UI-H-BW1-amr-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071079 /clone_end=3'	1	TTGTTTGTGTTTATTTATTTATTTTG AGGCAGCGTCTTGCTCTGTTGC
7759	db mining	Hs.320476	BF513187	11598368	UI-H-BW1-amj-e-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070155 /clone_end=3'	1	TGCCATCTTTACATCTAATCAAGAGG TAGAGCTTCCCTGGTGTCTCTGTC
7760	db mining	Hs.313828	AW453000	6993776	UI-H-BW1-ama-a-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069200 /clone_end=3'	1	TGCTCTGCTCTTCCCAATCAAGGAA TGTAGATCTTGCTAACAGAACTGC

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7761	db mining	Hs.120251	AA731386	2753542	nz86f07.s1 cDNA, 3' end /clone=IMAGE:1302373 /clone_end=3'	1	TGGCACCAACTTACACTTCCAGAAGA GAGTGGTTCAGGAAATTAATCTATGC
7762	db mining	Hs.313392	AW297908	6704544	UI-H-BW0-ajh-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732071 /clone_end=3'	1	AACTTTGGGAAGTGAGACTCTGTCTT GGGTTTTTGATAATAAATGTGGGC
7763	db mining	Hs.343320	BF512697	11597876	UI-H-BW1-amm-a-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070346 /clone_end=3'	1	CCGAGAAAGTACGGCTGGAGCGGAC TGGGGAGACGGAAATATTGAGTCGC
7764	db mining	Hs.304176	AI540182	4457555	td10f04.x1 cDNA, 3' end /clone=IMAGE:2075263 /clone_end=3'	1	CGAAGAAAGAATTGGATGCAGAAATTG TTGCCTAACCTGGGTGACAAGAGC
7765	db mining	Hs.320425	BF512629	11597808	UI-H-BW1-amm-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069700 /clone_end=3'	1	AGTGCCTGTGATTCCACCCCCCTTACC TCCCCTCAAGTGACAATGTAAGC
7766	db mining	Hs.313236	AW294711	6701347	UI-H-BW0-aim-b-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729806 /clone_end=3'	1	AGAAAGTTAGGAGTCGGCAACCTTAA GGAGGAGTTTCTATCATCTCTCC
7767	db mining	Hs.313379	AW297666	6704302	UI-H-BW0-ajh-c-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731755 /clone_end=3'	1	TGTCACAAAGATGAAGCAAGGTGGCT CAGGGAACGTGCTCAGAAACCTCC
7768	db mining	Hs.123341	AA810927	2880538	oa77d07.s1 cDNA, 3' end /clone=IMAGE:1318285 /clone_end=3'	1	GCAAAGTGAAAGTTTTCCCTTTGGCC CTAAATATGAAAGCAAGCATCC
7769	db mining	Hs.313208	AW293991	6700627	UI-H-BW0-alk-h-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729726 /clone_end=3'	1	CCCTGTCCATCTTTTCTGTCTCTATC CAGCCTTCCCTCTCTTTTGGCC
7770	db mining	Hs.123344	AA811024	2880635	oa82g05.s1 cDNA, 3' end /clone=IMAGE:1318808 /clone_end=3'	1	CCACGGAGGGCTCCCATCTAAAGG GAGTTTAATAACAAAGGAATGGCC
7771	db mining	Hs.320450	BF512839	11598018	UI-H-BW1-amu-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071322 /clone_end=3'	1	CAATTGGTACATTTCTCGGCAACCCCT TGCCACAAATTTCTCAGGAAGCC
7772	db mining	Hs.313369	AW297549	6704185	UI-H-BW0-aja-g-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731214 /clone_end=3'	1	AGGGTGTCCCTGTGATTTTAAATTC ACTATCTAGCTGTCCCTATCCCCC
7773	db mining	Hs.297527	BF515924	11601103	UI-H-BW1-aaa-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084001 /clone_end=3'	1	CTTATATTATGTTTTCTGTGACAAG CACCTCACCTCCCAACCCACCCC
7774	db mining	Hs.297513	BF515498	11600677	UI-H-BW1-ann-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082950 /clone_end=3'	1	GAGAAATCAAATTAATGCAGAGTCC TAGGCCACCCCTGGCATACCCACC
7775	db mining	Hs.105218	AA468881	2218483	aa55f06.s1 cDNA, 3' end /clone=IMAGE:824867 /clone_end=3'	1	ACAACCAATGCCTCACACTTAAGCTC CTAGAAGTCACTAGGGACCAAGACC
7776	db mining	Hs.309447	AI492062	4393065	tg12a11.x1 cDNA, 3' end /clone=IMAGE:2108540 /clone_end=3'	1	GCCCTCACCAGAATTCATCATGCTG GCACCTTATCTTGGACTTTCAACC
7777	db mining	Hs.309483	AI523758	4437893	tg94e10.x1 cDNA, 3' end /clone=IMAGE:2116458 /clone_end=3'	1	AGGGTAAGAGTTCAGACCTGACTG GACAATAAAGTGAGACTGTCTCTAC
7778	db mining	Hs.343333	BF515310	11600412	UI-H-BW1-ank-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082577 /clone_end=3'	1	CTCCGTCTGCCGCCCTCCGTAGCCAC AGCGACTTTTGAAGTGATATTGAC
7779	db mining	Hs.309687	AI401187	4244274	tg26h10.x1 cDNA, 3' end /clone=IMAGE:2109955 /clone_end=3'	1	CCCTGGAGAAGGAGGATGATTTATTT TCAACTTTCTGATTTACCAACCGAC
7780	db mining	Hs.314730	AI523958	4438093	tg98f08.x1 cDNA, 3' end /clone=IMAGE:2116839 /clone_end=3'	1	GATTGTTTGAGCCTGGGAGTTCACAC CCAGCCTGGGCTACATAGGGAGAC
7781	db mining	Hs.313337	AW297006	6703642	UI-H-BW0-ajf-c-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731409 /clone_end=3'	1	CTGCTCTAGACTGAGCACAGCCACTG ACAGGTGACCTTCAGAATCCTCAC
7782	db mining	Hs.116455	AA649141	2575570	ns32g12.s1 cDNA, 3' end /clone=IMAGE:1185382 /clone_end=3'	1	ACCCCTGCTTTACTGTGACAGACATA TAGTTTGTACATACATAAAACCCAC
7783	db mining	Hs.123313	AA810089	2879495	od12f12.s1 cDNA, 3' end /clone=IMAGE:1367759 /clone_end=3'	1	ACCTAACAGAAATTTGGATTGGGGTT GTCTAAATACACCTGGTGGGTTA
7784	db mining	Hs.319868	BF507353	11590660	UI-H-BW1-amm-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3071239 /clone_end=3'	1	GCCTTTCCCAACACAGTTTATGTGA TTCCCTGCCCTACCTTACCATT
7785	db mining	Hs.123342	AA811005	2880616	oa73g11.s1 cDNA, 3' end /clone=IMAGE:1317956 /clone_end=3'	1	TCCCATTTGCATGTCCCGTATATTGAA AGCTGCCTCTACTTCTCTCTGTA
7786	db mining	Hs.313288	AW296061	6702697	UI-H-BW0-aiu-g-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730802 /clone_end=3'	1	GGCAGGGGATGAACCAGATAATTTCC AGCCCTTCTTGGTAGCTCTCTGTA
7787	db mining	Hs.308998	AI356553	4108174	qz27h12.x1 cDNA, 3' end /clone=IMAGE:2028167 /clone_end=3'	1	GCTTAGGAGTTTGGGACCAGCCTGG GTAACATAGTGAAACCTGTCTCTA

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7788	db mining	Hs.313328	AW296796	6703432	UI-H-BW0-ajb-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731115 /clone_end=3'	1	TTGCAGCTATTTTCAAGTTGTAAGAAA TGAACCTTGCAACACATAGGGCTA
7789	db mining	Hs.320462	BF512988	11598165	UI-H-BW1-amh-c-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069707 /clone_end=3'	1	TCTCTTGCCACAGGGATTTCCTCCAA GCTGGAATCACCATTTCCTTCCTA
7790	db mining	Hs.297514	BF516300	11601479	UI-H-BW1-anz-e-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084010 /clone_end=3'	1	CCCACCCACCAGTAGGTTGTGATTCA ACTGAACCATTTTCAGGAGCACCTA
7791	db mining	Hs.124358	AA830650	2903749	oc52g02.s1 cDNA, 3' end /clone=IMAGE:1353362 /clone_end=3'	1	GAACCCAGCTAAGCCACACCCAGATT CTGACCCAGGGATACTCTGAAATA
7792	db mining	Hs.313345	AW297163	6703789	UI-H-BW0-ajd-a-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731279 /clone_end=3'	1	GTGTGTGCTGGCGTGCCTTATAGGT GTGCGTGTTTCCTGTCTAGTTTGA
7793	db mining	Hs.320484	BF513246	11598425	UI-H-BW1-amo-b-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070426 /clone_end=3'	1	AGGAAAACCTCAGAAATAATTTCTGCC CCCTGGATTCTCTAAGATTGTGA
7794	db mining	Hs.105130	AA482030	2209708	zu98g04.s1 cDNA, 3' end /clone=IMAGE:748070 /clone_end=3'	1	GTGGAAAGAATCTACACGAACACT ATTAAAGTCTGCACCTAGATCTGA
7795	db mining	Hs.104176	AA214530	1813155	zr92a06.s1 cDNA, 3' end /clone=IMAGE:683122 /clone_end=3'	1	GGCCTAGGTTCCAGCATTTCAGTCATC AAGTCTTGTTACAGAAATAAATGA
7796	db mining	Hs.121118	AA721101	2737236	nz67a01.s1 cDNA, 3' end /clone=IMAGE:1300488 /clone_end=3'	1	CCCCATTGGAGTCTAGTCAAAACAG CAGCTTCTTGAGTTACCATTTGGA
7797	db mining	Hs.313313	AW296455	6703091	UI-H-BW0-aig-c-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730224 /clone_end=3'	1	AAGGCTTGTAAGTGTAGGCCCTTGTA CTACACTGTGCTATACCTGGTAGA
7798	db mining	Hs.335116	AI524072	4438207	th01d07.x1 cDNA, 3' end /clone=IMAGE:2117005 /clone_end=3'	1	CACCTTGGGAGGCAGAGGTGAGCAG ATCACCTGAGGCCAGGAGTTTGAGA
7799	db mining	Hs.309130	AI382229	4195010	td04d04.x1 cDNA, 3' end /clone=IMAGE:2074663 /clone_end=3'	1	GGATCACTTGAAGCCAGCAGTTTGAG ACCAGCCTGGGCAATAAAATGAGA
7800	db mining	Hs.297504	BF514819	11599998	UI-H-BW1-anj-b-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3082338 /clone_end=3'	1	TCAGTTGTGATGGGATTCTTGATGG ATGAGATGTGTCGTGTGACAGAGA
7801	db mining	Hs.297473	BF513074	11598253	UI-H-BW1-amn-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070445 /clone_end=3'	1	CCTCTAGAACTGGAACCAAGACTGC TCCATCAGAGTTAAAGGTGTAAGA
7802	db mining	Hs.313168	AW292924	6699560	UI-H-BW0-aig-d-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729144 /clone_end=3'	1	GCTCACCCCTGCACCTCTTCCCAA TCTGCTGTACATTTTCTCAAAGA
7803	db mining	Hs.319885	BF507583	11590881	UI-H-BW1-ana-b-03-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071572 /clone_end=3'	1	TTCCTGTCTCCATGTTGTGGTCAAGA TTGCCATTTGCTTCTGAGTTTCA
7804	db mining	Hs.320411	BF512514	11597693	UI-H-BW1-amc-h-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069570 /clone_end=3'	1	CTGGTTCTAGTGCAGTCTCCTCACTT TCCTGGTGTGTTGTTATCTTTCA
7805	db mining	Hs.116501	AA651832	2583484	ns40b05.s1 cDNA, 3' end /clone=IMAGE:1186065 /clone_end=3'	1	TGACATGATTACCTGACTGATGTTTC TCCTCCATTAGACTGAATGCTTCA
7806	db mining	Hs.320438	BF512719	11597898	UI-H-BW1-amm-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070440 /clone_end=3'	1	TGGCAAAAAGCCCTAACACTGACTCAT CCCATTCTATCAGCACAAACTTCA
7807	db mining	Hs.319888	BF507612	11590910	UI-H-BW1-ana-e-12-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071734 /clone_end=3'	1	GTTTACAAGGGATACTAGTTCTCTGGA GGGACGAAGGAGGCTCTGTTTGCA
7808	db mining	Hs.250726	AW298545	6705181	UI-H-BW0-ajm-g-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732352 /clone_end=3'	1	TCCTCAACTCGGAGATTCTGTATGG AGAGAATCAATTTCTATATTTGCA
7809	db mining	Hs.120738	AA749236	2789194	nx99c09.s1 cDNA, 3' end /clone=IMAGE:1270384 /clone_end=3'	1	ACATTTCTTAGGTGTGTAGTGGTGAA GGAAAATAGTGGAAGATGTCTGCA
7810	db mining	Hs.320404	BF512350	11597616	UI-H-BW1-amc-b-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069264 /clone_end=3'	1	TCAGGAGGCTTGAAAAGACTCAAGGT TTCTACACTATGGGAAATAAGGCA
7811	db mining	Hs.319880	BF507510	11590808	UI-H-BW1-amr-c-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070831 /clone_end=3'	1	GTTTTCACTTGTGATACTAACTATTGT TTTTCTCCCCATGCCAAGAGCA
7812	db mining	Hs.320371	BF512091	11597303	UI-H-BW1-amf-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070208 /clone_end=3'	1	AGCCAAGGGAGCATATTATTCTCTTA TTTTAAACCTCTCCGTAGGCAGCA
7813	db mining	Hs.307837	AI052783	3308774	oy78h09.x1 cDNA, 3' end /clone=IMAGE:1672001 /clone_end=3'	1	AGAAGGACCCTGTTGAGAACCAC GGTTGTATAGAAAGGAATTGAAGCA
7814	db mining	Hs.124383	AA831706	2904805	oc85b04.s1 cDNA, 3' end /clone=IMAGE:1356463 /clone_end=3'	1	TTGACTGCCATAGCCAAGAGTTAATA TAGTTGCGTTTCTTAAGGAAGCA
7815	db mining	Hs.123304	AA809872	2879078	nz99b08.s1 cDNA, 3' end /clone=IMAGE:1303575 /clone_end=3'	1	CTTACTGTGCTTTTAGGTTTGTGTCT TTCTGTCTGTATGCTATGTCCA

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7816	db mining	Hs.123368	AA811539	2881150	ob45d08.s1 cDNA, 3' end /clone=IMAGE:1334319 /clone_end=3'	1	TGCAGTTAGGAGTGTGGACACTCTGC CCATCTCCATTGAATTAATCCCA
7817	db mining	Hs.313176	AW293164	6699800	UI-H-BW0-aii-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729448 /clone_end=3'	1	ACTTGGGTTCTATCCCCACGATAACT TGTTATGTATATGCCAATATCCCA
7818	db mining	Hs.313171	AW292976	6699612	UI-H-BW0-ah-b-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729055 /clone_end=3'	1	AGCTAGAAAATGTCCCTTTTTCTTCTT TGGAGGTCCTTTAACCAAGGCCCA
7819	db mining	Hs.343308	BF508886	11592184	UI-H-BI4-aos-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3085732 /clone_end=3'	1	ATCACCAATCTTATTTAGCACTGTGG ATGCCGTTTTGCAAAATGTCACCCA
7820	db mining	Hs.320468	BF513104	11598283	UI-H-BW1-amn-e-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070555 /clone_end=3'	1	TGACTTAAGGTTGGAATATCTCCTAC TACTCCCCTGTCTCCTTGACCA
7821	db mining	Hs.120585	AA743221	2782727	ny21c06.s1 cDNA, 3' end /clone=IMAGE:1272394 /clone_end=3'	1	TGTGGTTTGCAATGGTTTACTGATGA GACAGCAAAAATGAGACAGGACCA
7822	db mining	Hs.297468	BF513126	11598305	UI-H-BW1-amn-g-09-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070649 /clone_end=3'	1	TGGCGAGCCAGTCTCTGGATGGGAT TCTGATCAACAGAAGTTCTCATACA
7823	db mining	Hs.313205	AW293932	6700568	UI-H-BW0-alk-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729426 /clone_end=3'	1	TGCCCATCCTTTGCTGTTTTTCTCTTT CAGTCATGGCCTATTTGGAGACA
7824	db mining	Hs.343329	BF515646	11600825	UI-H-BW1-anu-d-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083555 /clone_end=3'	1	CTCAACCTTGGCCCTAAACTAACAGT GACAGGGAGTTCCTCAGCCTCACA
7825	db mining	Hs.319906	BF507755	11591053	UI-H-BW1-anc-g-07-0-UI.s2 cDNA, 3' end /clone=IMAGE:3072160 /clone_end=3'	1	TCCTGACCGTTGACAGAGAGCTTTTA CAGAAGTCTTAGGCAGTACACACA
7826	db mining	Hs.320465	BF513053	11598232	UI-H-BW1-amn-a-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070355 /clone_end=3'	1	AGTGTGTGGCACCAGGATCACTG TATGAGAAATTTCTGAACAACAACA
7827	db mining	Hs.320430	BF512667	11597846	UI-H-BW1-amg-f-06-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069850 /clone_end=3'	1	GCTGTAAGTCCCTTCCTTACTCATCT TCCCTCTCAAATACAACAACAACA
7828	db mining	Hs.120718	AA748539	2788497	ny05h12.s1 cDNA, 3' end /clone=IMAGE:1270919 /clone_end=3'	1	GCCAGTTGGCACCATTATGAAACAC ACCACCTTGTAACCACTGAATTAA
7829	db mining	Hs.320472	BF513154	11598333	UI-H-BW1-amj-b-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070011 /clone_end=3'	1	TCAACCTAGCACAGTGCCTGGCTGAT AGGTGTTGAATATTTCCACTCTAA
7830	db mining	Hs.319899	BF507695	11590993	UI-H-BW1-anb-h-05-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071865 /clone_end=3'	1	GCAACCCCTGCCCCCTGCAAAGAGAT ATTGTGACAAAGATATTCACTGAA
7831	db mining	Hs.124932	AA825273	2898575	oc67a02.s1 cDNA, 3' end /clone=IMAGE:1354730 /clone_end=3'	1	TAACATTCTGGCACAGTCCCTGGCA TAGGGTAGATAATAATGTTGGAA
7832	db mining	Hs.313354	AW297308	6703944	UI-H-BW0-aji-h-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2732020 /clone_end=3'	1	TCTCTAACCATCAAGGAAGGTCAAGG GCCATGTATCTCTTTTAGGAGAA
7833	db mining	Hs.127178	AA938725	3096753	oc10g07.s1 cDNA, 3' end /clone=IMAGE:1340508 /clone_end=3'	1	TTCCACAAACTCAGGTGTGCAAGAAA CAATGCATTACTTTATTTTCAGAA
7834	db mining	Hs.320445	BF512786	11597965	UI-H-BW1-amn-h-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070702 /clone_end=3'	1	CAGGAGTTTGAGACCAGCCTGGGCA ACATAGTAAGTCTCCATCTCTCAA
7835	db mining	Hs.319902	BF507708	11591006	UI-H-BW1-anc-b-02-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071930 /clone_end=3'	1	TCCCTAGTCTGGAGACTCGGGAAC AAAACAATCAATTCCTCCTGAGCAA
7836	db mining	Hs.104348	AA251338	1886301	zs08a06.s1 cDNA, 3' end /clone=IMAGE:684562 /clone_end=3'	1	TCCTCTTCATTGGAGACCCCTCCCTG TCACAGCACAATGTGGGTAATAAA
7837	db mining	Hs.320442	BF512761	11597940	UI-H-BW1-amn-f-08-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070598 /clone_end=3'	1	CAGAACAAAGGCCACAGTGTGAAAG GTGCTGCTGAACAAGATAAATAAA
7838	db mining	Hs.320470	BF513152	11598331	UI-H-BW1-amj-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069983 /clone_end=3'	1	GAGTCAGCAACTGTGCTCTCTTGC TTGGTTGATGCTTTTGAAGTAA
7839	db mining	Hs.300359	BF516423	11601602	UI-H-BW1-aob-h-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:3084512 /clone_end=3'	1	TAAGGATGTATCCCTATGGGCAGGAA ACCCAATTCTAAGAACTTACAAA
7840	db mining	Hs.309152	AI392970	4222517	tg22d05.x1 cDNA, 3' end /clone=IMAGE:2109513 /clone_end=3'	1	GCCACTGCACTCCAGCCTGGGCAAC AGAGCGAGACCTTGACTCTTAAAA
7841	db mining	Hs.122448	AA761767	2810697	nz31e08.s1 cDNA, 3' end /clone=IMAGE:1289414 /clone_end=3'	1	CACAACACCCAAAGGCTGCATTGCA TAACATGTATTTGTTGAATGAAAA
7842	db mining	Hs.319874	BF507452	11590750	UI-H-BW1-amz-e-06-0-UI.s2 cDNA, 3' end /clone=IMAGE:3071699 /clone_end=3'	1	GGGGTCTTGCTCACAGAGCTCCCA AGATGGTGGTGGGCCACTTCAAAA
7843	db mining	Hs.104177	AA214542	1813157	zr92b09.s1 cDNA, 3' end /clone=IMAGE:683129 /clone_end=3'	1	TCCCTCTATAGGTAAAGACCTGTTT GTCTGAAATGTGTGGAACCTGTCT

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7844	db mining	Hs.104182	AA521405	2261948	aa68c06.s1 cDNA, 3' end /clone=IMAGE:826090 /clone_end=3'	1	GCTGCCGTGTCTTTTGGCATTTCAG CATGACTATATGTTTTGTAATGT
7845	db mining	Hs.255522	AW296182	6702818	UI-H-B12-ala-c-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:2728680 /clone_end=3'	1	CCGAAGGCCCGTGTGGCGCTTCTCC TATTCTGTAGAGTGGTAGTTTGTTT
7846	db mining	Hs.124928	AA765668	2816906	oa04f02.s1 cDNA, 3' end /clone=IMAGE:1303995 /clone_end=3'	1	AAAGAGGTAACGCAAGTTCTCTCTT GTAGGTGGGCTACAGGTGACTTT
7847	db mining	Hs.320388	BF512314	11597493	UI-H-BW1-amb-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069453 /clone_end=3'	1	TGGTTCTCAGCCTGGGTGAACAGAG AAGGGGTCTAATTGGTCTTTTGTT
7848	db mining	Hs.123161	AA807319	2876895	oc38b01.s1 cDNA, 3' end /clone=IMAGE:1351945 /clone_end=3'	1	TGTTCTTGGCACCCCTGCAGTGTGAGG CTATATCATTTCTGTTTGTTCTT
7849	db mining	Hs.120608	AA743877	2783228	ny25b04.s1 cDNA, 3' end /clone=IMAGE:1272751 /clone_end=3'	1	TCTCATTTTCTTTTCTAGCTGTGATG CAAAGTGTGAGTGGTCCCATCTT
7850	db mining	Hs.120554	AA741010	2779602	ny99a10.s1 cDNA, 3' end /clone=IMAGE:1286394 /clone_end=3'	1	TGTCCAACCTTCTTTTGCTACAAAC AAAGAATGCCTAGGGATTCAACTT
7851	db mining	Hs.330148	BE676227	10036768	xm80f05.x1 cDNA, 3' end /clone=IMAGE:2690529 /clone_end=3'	1	CAAGTGGCCTTGGTGTAAATCTTG CCCTAAATTGTAACACATGATT
7852	db mining	Hs.120259	AA731522	2753878	nw59h09.s1 cDNA, 3' end /clone=IMAGE:1250945 /clone_end=3'	1	ACCAACCAAGTGGTGTGCTGGAGCTG TCTCATACTATCTTGAGAGTCCATT
7853	db mining	Hs.124333	AA829233	2902332	od05a10.s1 cDNA, 3' end /clone=IMAGE:1358298 /clone_end=3'	1	AGCACTTGCTTTTGTCCAGACATTGT CCTTAGCTCCTTTCTTGTAATT
7854	db mining	Hs.124281	AA825840	2899152	od59d02.s1 cDNA, 3' end /clone=IMAGE:1372227 /clone_end=3'	1	TGCAGCAAAATTTGAATTTTCATAGGC CATTCAAGTGTCTCTGCGATAATT
7855	db mining	Hs.120716	AA748500	2788458	ny01h10.s1 cDNA, 3' end /clone=IMAGE:1270531 /clone_end=3'	1	CCAGGAATGGAATACGCCAACCCCA GGTTAGGCACCTCTATTGCAGAATT
7856	db mining	Hs.320428	BF512663	11597842	UI-H-BW1-amb-g-02-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069842 /clone_end=3'	1	AGGAAATTTGGTTGAAGTCGTTTTCT CTTGTTAGTCTCATGTTAAGCTGT
7857	db mining	Hs.123593	AA814828	2884424	ob73d07.s1 cDNA, 3' end /clone=IMAGE:1337005 /clone_end=3'	1	TGCCTGGGGGAGAATTTAAATCTAA GTCGCTGGAAGTCCCTTTGTATGT
7858	db mining	Hs.120214	AA730985	2752189	nw67a04.s1 cDNA, 3' end /clone=IMAGE:1251630 /clone_end=3'	1	ACCTGTAGGAAGGGTTTGTAATATT CTGTTGCTCTGAATTATTAGCGGT
7859	db mining	Hs.123365	AA811469	2881080	ob83c11.s1 cDNA, 3' end /clone=IMAGE:1337972 /clone_end=3'	1	TGAGAGGATCTTGAGACATTCTTGTT TTATTTGCCCTCTATGTTTAGGT
7860	db mining	Hs.127156	AA838155	3096268	oc10a09.s1 cDNA, 3' end /clone=IMAGE:1340440 /clone_end=3'	1	TCCCAAGCATGAGACAAGTACCACCA GTGGTTCAAGAGATGATTTTAGGT
7861	db mining	Hs.320486	BF513276	11598455	UI-H-BW1-amo-e-01-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070560 /clone_end=3'	1	ACAAGACAGCAGCCTTCCCGAAATGT CACTACTAAGAATTATTCAGAGGT
7862	db mining	Hs.343330	BF514718	11599897	UI-H-BW1-ans-a-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3083063 /clone_end=3'	1	GCTGCCCAAACTTCCATTTATTTACC CTCCAACATCACTTCCTTCTCT
7863	db mining	Hs.123584	AA814349	2883945	nz08h08.s1 cDNA, 3' end /clone=IMAGE:1287035 /clone_end=3'	1	ACATTTGCCAATGCACCTTGATGTAAA GTTGTTGAGGATGTTGACTCTCCT
7864	db mining	Hs.123376	AA811751	2881362	ob80e12.s1 cDNA, 3' end /clone=IMAGE:1337710 /clone_end=3'	1	TCCCCCTTCTAACACCAATTTGGGA ACATCACTACTTGATATTATCCT
7865	db mining	Hs.122860	AA766374	2817612	oa36b03.s1 cDNA, 3' end /clone=IMAGE:1307021 /clone_end=3'	1	TCAAGACCCTTAGAGTAAGTTAACTC CCAAGGAAATGTAGTTAGTCCCT
7866	db mining	Hs.105268	AA490812	2219985	aa49e05.s1 cDNA, 3' end /clone=IMAGE:824288 /clone_end=3'	1	AACCCACAATCCAACCTCCCTTGATGA GGATGATCATTAAACAACATCACT
7867	db mining	Hs.297465	BF512677	11597856	UI-H-BW1-amb-g-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069894 /clone_end=3'	1	TTTGAAGCCTCTGGTACTTCCCTTTC CCAAACCCAGTCACAGGAAACACT
7868	db mining	Hs.127167	AA938326	3096437	oc11c08.s1 cDNA, 3' end /clone=IMAGE:1340558 /clone_end=3'	1	TTGGAGGTTAACAGTATTCCTTTGAG TGGTGTGATTAAAGGTGCTTTTAT
7869	db mining	Hs.123361	AA811359	2880970	ob82a07.s1 cDNA, 3' end /clone=IMAGE:1337844 /clone_end=3'	1	CCAACCTCCAGAACTGCCTATCTAAC TCATCTGTGGTGATGGAATGCTAT
7870	db mining	Hs.105282	AA491247	2220420	aa49b01.s1 cDNA, 3' end /clone=IMAGE:824233 /clone_end=3'	1	AGTGCTCTCTGCTGTTAGCATGGTT ACTAATCTTTTGGTTACTTTTCAT
7871	db mining	Hs.320385	BF512292	11597471	UI-H-BW1-amb-d-12-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069359 /clone_end=3'	1	TGACCTCAGTGTCTACTTCAGCAGAA CCTGTGGGTATATGCCTACCTCAT

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7872	db mining	Hs.105506	AA521196	2261739	aa74c04.s1 cDNA, 3' end /clone=IMAGE:826662 /clone_end=3'	1	AAGGAGAACTGTCAACTGAATCTCAA ATGCAGTCAAATGAAGAGAGGCAT
7873	db mining	Hs.124928	AA765759	2816997	oa07h05.s1 cDNA, 3' end /clone=IMAGE:1304313 /clone_end=3'	1	TTCAAGTCATTATAGGTTTGGGCATA CAGGGTTAACCTTGATGTACAT
7874	db mining	Hs.320488	BF513286	11598465	UI-H-BW1-amo-e-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070580 /clone_end=3'	1	AGCAGAACACATGTGTTTGACACTT TTCCTTCTCTGTAATGAGGTACAT
7875	db mining	Hs.122891	AA767801	2818816	oa45h09.s1 cDNA, 3' end /clone=IMAGE:1307969 /clone_end=3'	1	TGCCTGTGTGGGTCAAAGGAATCATC TATGCTAATGTATTTGAGCCAAAT
7876	db mining	Hs.116435	AA648285	2574714	ns20d12.s1 cDNA, 3' end /clone=IMAGE:1184183 /clone_end=3'	1	ACCGAAAGCAGCATTTTCAATGTTTA ATTAATCGATGCAGGAAATTGTG
7877	db mining	Hs.300303	AW292760	6699396	UI-H-BW0-ajl-c-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729453 /clone_end=3'	1	GTCCCTGGCCCTTCACTCTTCGTCCA GGCTCTCTGACCTCTTCCCTCTG
7878	db mining	Hs.123154	AA688058	2674964	nv58c04.s1 cDNA, 3' end /clone=IMAGE:1233990 /clone_end=3'	1	TGTCCGCTGTTTTACCTCACTGCTCC TGTTTATGCCCTTAACCTCTGCTG
7879	db mining	Hs.320489	BF513296	11598475	UI-H-BW1-amo-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070628 /clone_end=3'	1	GCACAAGACCTCACTTGGAAACAAGTA CCAGGCAGAAAGAGACATTACCTG
7880	db mining	Hs.124353	AA830448	2903547	oc51d05.s1 cDNA, 3' end /clone=IMAGE:1353225 /clone_end=3'	1	TTTCATATCTTGGCAGTTGGATGCGG TAAGAGCCACAGAGAAACCACTG
7881	db mining	Hs.122824	AA765319	2816557	oa01f11.s1 cDNA, 3' end /clone=IMAGE:1303725 /clone_end=3'	1	AGGACCCCTTTCCCATATTTCTGGCT ATATACAAGGATATCCAGACACTG
7882	db mining	Hs.124317	AA827178	2901175	ob53g04.s1 cDNA, 3' end /clone=IMAGE:1335126 /clone_end=3'	1	ACCAGGCCTAGAAATTAGGTTCTAGG TGTAACCTATTGGCCTATCAGATG
7883	db mining	Hs.300373	AW297820	6704445	UI-H-BW0-aiy-h-04-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731230 /clone_end=3'	1	GTGCATTTTAGCAACAGACTTCCAGG TTTCAGCGCGGGGCCAGGAAGGGG
7884	db mining	Hs.320464	BF513050	11598229	UI-H-BW1-amn-a-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070349 /clone_end=3'	1	CTGTCATGCACCACCTCATCCCTCC TTCAGGGCCAGGGAGAGTCCCTAG
7885	db mining	Hs.313366	AW297537	6704173	UI-H-BW0-aja-f-05-0-UI.s1 cDNA, 3' end /clone=IMAGE:2731160 /clone_end=3'	1	AGAGGAGGAGGGGGTAGAATGAATT TCATTTAAAGCTCAACCTAGTTCAAG
7886	db mining	Hs.320427	BF512648	11597827	UI-H-BW1-amg-d-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069762 /clone_end=3'	1	CAGTCTCCAGCTTTCTTGGCCTCCT CTGCCAAGCTGGATGCAAGGCTCAG
7887	db mining	Hs.252840	AW015143	5863980	UI-H-Blop-abb-e-07-0-UI.s1 cDNA, 3' end /clone=IMAGE:2711149 /clone_end=3'	1	TGGAGAGAAGGTTCCGGGAAGACGAG GGGGCTGGGAGGTTTGGAAAGACAG
7888	db mining	Hs.313161	AW292801	6699437	UI-H-BW0-ajl-f-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:2729613 /clone_end=3'	1	CTGAAATGGGGGAAGGTGGGTTATG ACAAAGTTCATGGAGAGGCTGAAG
7889	db mining	Hs.309124	AI380478	4190331	tf95a09.x1 cDNA, 3' end /clone=IMAGE:2107000 /clone_end=3'	1	TAAAGCGGTACGGGATTCGCCACCC TACTCCAGCAAGAAAGAGCCTGAAG
7890	db mining	Hs.120562	AA741098	2779688	ny99g07.s1 cDNA, 3' end /clone=IMAGE:1286480 /clone_end=3'	1	AGCATTCATTCTCCAAACACACTCC CAGGGTTAGGTCTCTTACCTCTGC
7891	db mining	Hs.105530	AA521450	2261993	aa69d11.s1 cDNA, 3' end /clone=IMAGE:826197 /clone_end=3'	1	GGTGTGAATATTTATACGGATTGGC ATCATAAGATACCGGATACCTGC
7892	db mining	Hs.123194	AA805997	2874747	oc18g05.s1 cDNA, 3' end /clone=IMAGE:1341272 /clone_end=3'	1	ACCTTAGTCTAACTGCCTTCTGTAAA GTGGGTTGCTATAGTCTTTAAGCC
7893	db mining	Hs.122833	AA765597	2816835	oa08a10.s1 cDNA, 3' end /clone=IMAGE:1304346 /clone_end=3'	1	TGAGGTTTGATGTTGGCAGGTAAAA CAGAAAGGCAAGATGTCATCTGAC
7894	db mining	Hs.313827	AW452984	6993760	UI-H-BW1-amd-g-11-0-UI.s1 cDNA, 3' end /clone=IMAGE:3069525 /clone_end=3'	1	TGGAGCTGCTACATAATTATTTACAGG TCTCAAAGCTTCCAAGAAGTGGAC
7895	db mining	Hs.122383	AA789140	2849260	aa66g10.s1 cDNA, 3' end /clone=IMAGE:825954 /clone_end=3'	1	AGACGGAACCTGAGATGTTGGATGTT GTTGATCTTAGCAACAGACTTTA
7896	db mining	Hs.120226	AA731687	2752576	nw58f05.s1 cDNA, 3' end /clone=IMAGE:1250817 /clone_end=3'	1	AGATCTGTAATCTTTGGCAAATGGAA CTCACCTGCAACGATACCTACTTA
7897	db mining	Hs.120288	AA731998	2753949	nw61b04.s1 cDNA, 3' end /clone=IMAGE:1251055 /clone_end=3'	1	GAGGACTTCCATTCCCATTTCCCGC ATACCTGCTGTTCTGTCTGAATTA
7898	db mining	Hs.123168	AA804519	2873650	ns28a11.s1 cDNA, 3' end /clone=IMAGE:1184924 /clone_end=3'	1	AGCTCACACCTGTTCCCTTCATGGGTC AGTTCCTTTCAATTTTCACTTTTGA
7899	db mining	Hs.124369	AA830835	2903934	oc54b06.s1 cDNA, 3' end /clone=IMAGE:1353491 /clone_end=3'	1	AGCTGCTGCTTCTCTTTCAGTTGCAA ATGCAACCTGTTATAATCTTTGA

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7900	db mining	Hs.122482	AA767335	2818350	nz65h02.s1 cDNA, 3' end /clone=IMAGE:1300371 /clone_end=3'	1	TCAATATCTGTGTCTTTTCATGAGT GGCTGTTACTTGTGAAGAATTGA
7901	db mining	Hs.313287	AW296059	6702695	UI-H-BW0-alu-g-03-0-UI.s1 cDNA, 3' end /clone=IMAGE:2730798 /clone_end=3'	1	TGAGTGGACTGAGGAATGAATAGAAA ACGTGATATATGTAGAAAGCTGA
7902	db mining	Hs.120705	AA748015	2787973	nx87c05.s1 cDNA, 3' end /clone=IMAGE:1269224 /clone_end=3'	1	ACCAGCCCCTGGGAATGTTATGAGCA AATGATACTCCATGAGTAAATGA
7903	db mining	Hs.320495	BF513385	11598584	UI-H-BW1-amk-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070242 /clone_end=3'	1	TCGTGTGAGTGTGAGAGACATGTTCA TTGTGAAAAGATACTCCTAGTGGA
7904	db mining	Hs.121104	AA721020	2737155	nx89f11.s1 cDNA, 3' end /clone=IMAGE:1269453 /clone_end=3'	1	TTTGTCAAATGCCTGTTCCACCATCTG TGGAAGTCATTATATGATTCAGGA
7905	db mining	Hs.124297	AA827809	2900172	od08c04.s1 cDNA, 3' end /clone=IMAGE:1367334 /clone_end=3'	1	ACACTTTTCTTCTAAGGAGAGCTTTCT TAGGCATTTCAAAGAACTTTCGA
7906	db mining	Hs.320372	BF512098	11597308	UI-H-BW1-ami-f-10-0-UI.s1 cDNA, 3' end /clone=IMAGE:3070218 /clone_end=3'	1	ACCAAATGAGTACCATCTGTTGAACA CAGGGTGGCGATCCAAGTGTTTCA
7907	HUVEC cDNA	Hs.92381	AB007956	3413930	mRNA, chromosome 1 specific transcript KIAA0487 /cds=UNKNOWN	1	ACCTGACTTCCACGATAAAATGGAGA TGAGTGCAGGGGTGAGTGATATAGT
7908	HUVEC cDNA	Hs.24950	AB008109	2554613	regulator of G-protein signalling 5 (RGS5), mRNA /cds=(81,626)	1	TGCAGATTTATACTCCTGACGTGTCT CATTACACAGCTAAATAATAGGCCA
7909	HUVEC cDNA	Hs.306193	AB011087	3043553	hypothetical protein (LQFBS-1), mRNA /cds=(0,743)	1	ACCCTCGCCCTTCCCTCCGGTTCAG TACCTATTGTTTCTCCTTTCAAAT
7910	HUVEC cDNA	Hs.154919	AB014525	3327063	mRNA for KIAA0625 protein, partial cds /cds=(0,2377)	1	AAGAGGAAATGGCAGAAATTAAGCA GAAACAAGAAGATGGACATGGATT
7911	HUVEC cDNA	Hs.153026	AB014540	3327093	mRNA for KIAA0640 protein, partial cds /cds=(0,1812)	1	AAGAGTGTGTGAGTGCTGTGATCAG GTGTTTTCCTTAATAAGTAGGGAT
7912	HUVEC cDNA	Hs.24439	AB014546	3327105	ring finger protein (C3HC4 type) 8 (RNF8), mRNA /cds=(112,1569)	1	CTGCTGTCCACTTTCCTTCAGGCTCT GTGAATACTTCAACCTGCTGTGAT
7913	HUVEC cDNA	Hs.155829	AB014576	3327165	mRNA for KIAA0876 protein, partial cds /cds=(0,3789)	1	TTCTTGGATTCACTTTCAGTTGGCTA GAAATTACACTGTGCTCAATGCCT
7914	HUVEC cDNA	Hs.93675	AB022718	4204189	decidual protein induced by progesterone (DEPP), mRNA /cds=(218,856)	1	AGGTCTCTGCCACCTCCTTCTCTGTG AGCTGTCAGTCTAGGTATTCTCT
7915	HUVEC cDNA	Hs.104305	AB023143	4589483	death effector filament-forming Ced-4- like apoptosis protein (DEFCAP), transcript variant B, mRNA /cds=(522,4811)	1	GAATAGGAGGGACATGGAACCATTTG CCTCTGGCTGTGTACAGGGTGAG
7916	HUVEC cDNA	Hs.103329	AB023187	14133226	KIAA0970 protein (KIAA0970), mRNA /cds=(334,2687)	1	CCTGTTTAAGAAAGTGAAATGTTATG GTCTCCCCTCTTCCAATGAGCTTA
7917	HUVEC cDNA	Hs.155182	AB028959	5689408	KIAA1036 protein (KIAA1036), mRNA /cds=(385,1482)	1	TTTCACTTTCACACTTCATCTCATTCC TGTTGTCACTTTCCCCGAAACGA
7918	HUVEC cDNA	Hs.129218	AB028997	5689484	DNA sequence from clone RP11- 145E8 on chromosome 10. Contains the gene KIAA1074, the 3' end of the YME1L1 gene for YME1 (<i>S.cerevisiae</i>)- like 1, ESTs, STSs, GSSs and a CpG island /cds=(166,5298)	1	TCTGGATCAATAGCTTCCCCTCTAGG GTCTACTGATGAGTCAAACTTAA
7919	HUVEC cDNA	Hs.8383	AB032255	6683499	bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA /cds=(366,6284)	1	TTTATCTACTGTGTGTTGTGGTGGCC TGTTGGAGGCAATAGATCAGATT
7920	HUVEC cDNA	Hs.15165	AB037755	7243048	novel retinal pigment epithelial gene (NORPEG), mRNA /cds=(111,3053)	1	GACATTTTGTAGGATGCCTGACGAG GTGTAGCCTTTTATCTTGTTCCTG
7921	HUVEC cDNA	Hs.82113	AB049113	10257384	dUTP pyrophosphatase (DUT), mRNA /cds=(29,523)	1	CCCAGTTTGTGGAAGCACAGGCAAG AGTGTTCTTTTCTGGTGATTCTCCA
7922	HUVEC cDNA	Hs.8180	AF000652	2795862	syndecan binding protein (syntenin) (SDCBP), mRNA /cds=(148,1044)	1	TGTTCCCTTTTCTGACTCCTCCTTGC AAACAAAATGATAGTTGACACTTT
7923	HUVEC cDNA	Hs.147916	AF000982	2580549	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(856,2844)	1	GTGACTTGATACATTCAGCAATAGCAT TTGAGCAAGTTTATCAGCAAGCA
7924	HUVEC cDNA	Hs.75058	AF002163	2290769	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA /cds=(209,3547)	1	TTGCTATCGACATTCCTCGTATAAGA GAGAGACATATCACGCTGCTGCA
7925	HUVEC cDNA	Hs.42915	AF006082	2282029	ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA /cds=(74,1258)	1	CCTGCCAGTGTGAGAAAATCCTATTT ATGAATCCTGTGGTATTCTTTGG
7926	HUVEC cDNA	Hs.11538	AF006084	2282033	actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1B), mRNA /cds=(80,1198)	1	AGGGAGGGGACAGATGGGGAGCTTT TCTTACCTATTCAAGGAATACGTGC
7927	HUVEC cDNA	Hs.6895	AF006086	2282037	actin related protein 2/3 complex, subunit 3 (21 kD) (ARPC3), mRNA /cds=(25,581)	1	TCAAGAATTGGGTGGGAGAAAAGAA AGTGGGTTATCAAGGGTGATTTGA
7928	HUVEC cDNA	Hs.286027	AF010313	6468761	etoposide-induced mRNA (PIG8), mRNA /cds=(72,1151)	1	TGTGATTAGGTTGTTTCTGTGCTTTT TTGAGAGACTAAAATTGTGGGGG

Table 8

7929	HUVEC cDNA	Hs.79150	AF026291	2559007	chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA /cds=(0,1619)	1	TGGGCTTGGTCTTCCAGTTGGCAATT GCCTGAAGTTGTATTGAAACAATT
7930	HUVEC cDNA	Hs.81452	AF030555	3158350	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(508,2641)	1	AACAAGATGAGAACAGATAAAGATTG TGTGGTGTITTTGGATTGGAGAGA
7931	HUVEC cDNA	Hs.139851	AF035752	2665791	caveolin 2 (CAV2), mRNA /cds=(20,508)	1	TGTAGCTCCCAAGGTAAACTTCAT TGGTAAGATTGCACGTCTCTGATT
7932	HUVEC cDNA	Hs.194709	AF037364	14030860	paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(664,1725)	1	TCACTCCCCATTTTCATTTCTTGTC GAGAATAGTTCTTGTCTCATACTG
7933	HUVEC cDNA	Hs.79516	AF039656	2773159	brain acid-soluble protein 1 (BASP1), mRNA /cds=(52,735)	1	TGGGAGTGACAAACATTTCTCAATCC TACTTAGCCTACCTAGATTCTCA
7934	HUVEC cDNA	Hs.29417	AF039942	4730928	HCF-binding transcription factor Zhangfei (ZF), mRNA /cds=(457,1275)	1	AATGGAAGGATTAGTATGGCCTATTT TTAAAGCTGCTTTGTAGTTCTCT
7935	HUVEC cDNA	Hs.26232	AF044414	6136293	mannosidase, alpha, class 2C, member 1 (MAN2C1), mRNA /cds=(58,3244)	1	CCCCAGCCTAAGCAGGGATCAGTC TTTTCTGTGGAATAAATCCTTGA
7936	HUVEC cDNA	Hs.3776	AF062072	3668065	zinc finger protein 216 (ZNF216), mRNA /cds=(288,929)	1	TGTGGTAATGCCTGTTTTTCATCTGTA AATAGTTAAGTATGTACACGAGGC
7937	HUVEC cDNA	Hs.74034	AF070648	3283922	clone 24651 mRNA sequence /cds=UNKNOWN	1	AGATGCTTAGTCCCTCATGCACATCA ATTACTGGTCCAAAAGATTGCTGA
7938	HUVEC cDNA	Hs.274230	AF074331	5052074	PAPS synthetase-2 (PAPSS2) mRNA, complete cds /cds=(63,1907)	1	AAAACCTGCTTCTGCTCTAGTACCA TGCTTAGTGCAAAATGATTATTTCT
7939	HUVEC cDNA	Hs.12540	AF081281	3415122	lysophospholipase 1 (LYPLA1), mRNA /cds=(35,727)	1	AGCTATTAGGATCTTCAACCCAGGTA ACAGGAATAATTCTGTGGTTTCAT
7940	HUVEC cDNA	Hs.159629	AF092131	5138911	myosin IXB (MYO9B), mRNA /cds=(0,6068)	1	TCCTGCGTCTATCCATGTGGAAATGCT GGACAATAAAGCGAGTGCTGCCCA
7941	HUVEC cDNA	Hs.273385	AF105253	7532779	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (GNAS1), mRNA /cds=(68,1252)	1	GCCACAAAAGTTCCCTCTCACTTTCA GTAAAAATAAATAAACAGCAGCA
7942	HUVEC cDNA	Hs.2934	AF107045	5006419	ribonucleotide reductase M1 polypeptide (RRM1), mRNA /cds=(187,2565)	1	ACTGCTTTGACTGGTGGGTCTCTAGA AGCAAACTGAGTGATAACTCATG
7943	HUVEC cDNA	Hs.158237	AF112345	6650627	integrin alpha 10 subunit (ITGA10) mRNA, complete cds /cds=(78,3579)	1	GGCATTGTCTCTGTTTCCAGTGGGG TGACAGTATATCAGATGGTCAGA
7944	HUVEC cDNA	Hs.183698	AF116627	7959755	ribosomal protein L29 (RPL29), mRNA /cds=(29,508)	1	CCCTGGGTACCATCTGCATGGGGC TGGGGTCTCTGTGCTATTTGTAC
7945	HUVEC cDNA	Hs.2186	AF119850	7770136	Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501 IMAGE:2964623, mRNA, complete cds /cds=(2278,3231)	1	TCAAGTGAACATCTCTGCCATCACC TAGCTGCCTGCACCTGCCCTTCAG
7946	HUVEC cDNA	Hs.22900	AF134891	7381111	nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA /cds=(492,1694)	1	TCTTGGCAGCCATCCTTTTAAAGAGT AAGTTGGTTACTTCAAAAGAGCA
7947	HUVEC cDNA	Hs.108258	AF141968	6273777	actin cross-linking factor (ACF7), transcript variant 1, mRNA /cds=(51,18343)	1	AGCTAAAGAGAGGGAACCTCATCTAA GTAACTTTGCACATGATACAGCA
7948	HUVEC cDNA	Hs.11156	AF151072	7106865	hypothetical protein (LOC51255), mRNA /cds=(0,461)	1	GCTGAGTGCTGGCCCTCTGCGTCTT CCTTATTAACCTTGAATCCTCATTA
7949	HUVEC cDNA	Hs.179573	AF193556	6907041	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(139,4239)	1	TGAATGATCAGAACTGACATTTAATTC ATGTTTGTCTCGCCATGCTTCTT
7950	HUVEC cDNA	Hs.41135	AF205940	8547214	endomucin-2 (LOC51705), mRNA /cds=(78,863)	1	TCCGGGCCAAGAATTTTATCCATGA AGACTTTCTCTACTTTCTCGGTGT
7951	HUVEC cDNA	Hs.142908	AF219119	7158848	E2F-like protein (LOC51270), mRNA /cds=(278,979)	1	GCAGAGTTCATTGTTGCCCTTAACA GTTTTCTCTGAGTTTACTGAAGAA
7952	HUVEC cDNA	Hs.154721	AF261088	9802307	aconitase 1, soluble (ACO1), mRNA /cds=(107,2776)	1	TTATCAAGCAGAGACCTTTGTTGGGA GGCGGTTTGGGAGAACACATTTCT
7953	HUVEC cDNA	Hs.76288	AF261089	9802309	calpain 2, (mII) large subunit (CAPN2), mRNA /cds=(142,2244)	1	GGGTATGCTGCCTCTGTAAATTCATG TATTCAAAGGAAAAAGACACCTTGC
7954	HUVEC cDNA	Hs.152707	AJ001259	2769253	glioblastoma amplified sequence (GBAS), mRNA /cds=(8,868)	1	TTGCTGCCCAATCAAGAATGTA TGTGTAAGTGTGAATAAATCTCA
7955	HUVEC cDNA	Hs.5097	AJ002308	2959871	synaptogyrin 2 (SYNGR2), mRNA /cds=(29,703)	1	ATGCCCGGCTGGGATGCTGTTTGG AGACGGAATAAATGTTTCTCATTC
7956	HUVEC cDNA	Hs.143323	AJ243706	6572290	mRNA for RB-binding protein (rbp2h1a gene) /cds=(757,5802)	1	AGCAGTTTGTGATATAGCAGAGGTTT AAATGTACCCCTCCCTTTTATGCA
7957	HUVEC cDNA	Hs.1197	NM_002157	4504522	Heat shock 10kD protein 1 (chaperonin 10)	1	TGATGCTGCCCATTCCTAGAGTTTC TGAAATCTTTCGTATGTAATAA
7958	HUVEC cDNA	Hs.79037	BC010112	14603308	Homo sapiens, heat shock 60kD protein 1 (chaperonin), clone MGC:19755 IMAGE:3630225, mRNA, complete cds /cds=(1705,3396)	1	AGCAGCCTTCTGTGGAGAGTGAGAA TAATTGTGTACAAAGTAGAGAAGT
7959	HUVEC cDNA	Hs.279860	AJ400717	7573518	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(94,612)	1	CATCTGAAGTGTGGAGCCTTACCCAT TTCATCACCTACAACGGAAGTAGT

Table 8

7950	HUVEC cDNA	Hs.165563	AK024508	10440535	DNA sequence from clone RP4-591C20 on chromosome 20. Contains ESTs, STSs, GSSs and CpG islands. Contains a novel gene for a protein similar to NG26, the TPO52L2 gene for two isoforms of tumor protein D52-like protein 2, a gene for a novel DnaJ domain protein similar to mouse and bovine cysteine string protein with two isoforms, a gene for a novel phosphoributokinase with three isoforms, the KIAA1196 gene and the 5' part of the TOM gene for a putative mitochondrial outer membrane protein import receptor similar to yeast pre-mRNA splicing factors Prp1/Zer1 and Prp6 /cds=(0,503)	1	GCCAGGCTGGTTCGCATGGTGATC TCCGTCCTGTATGTCTGAATGTTGG
7961	HUVEC cDNA	Hs.91146	AL050147	4884153	protein kinase D2 mRNA, complete cds /cds=(39,2675)	1	CTATTTCCAAGGCCCTCCCTGTTTC CCCAGCAATTAAACGGAATCATC
7962	HUVEC cDNA	Hs.66762	AL050367	4914600	mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) /cds=UNKNOWN	1	AAAGTGCCAGAATGACTCTTCTGTGC ATTCTTCTAAAGAGCTGCTTGGT
7963	HUVEC cDNA	Hs.165998	AL080119	5262550	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(85,1248)	1	TTGTTGGTAGGCACATCGTGTCAAGT GAAGTAGTTTTATAGGTATGGGTT
7964	HUVEC cDNA	Hs.111801	AL096723	5419856	mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023) /cds=UNKNOWN	1	AGTCCTGTATCATCCACTTGTACTA CCTTGCTCTATGAAGCTCTGAGA
7965	HUVEC cDNA	Hs.89434	AL110225	5817161	drebrin 1 (DBN1), mRNA /cds=(97,2046)	1	TTGGCCGCTTCCCTACCCACAGGGC CTGACTTTTACAGCTTTTCTCTTTT
7966	HUVEC cDNA	Hs.7527	AL110239	5817182	small fragment nuclease (DKFZP586E144), mRNA /cds=(77,790)	1	TATGACACAGCAGCTCCTTTGTAAGT ACCAGGTCATGTCCATCCCTTGGT
7967	HUVEC cDNA	Hs.187991	AL110269	5817043	DKFZP564A122 protein (DKFZP564A122), mRNA /cds=(2570,2908)	1	TTGGTGAGTTGCCAAAGAAGCAATAC AGCATATCTGCTTTTGCCTTCTGT
7968	HUVEC cDNA	Hs.25882	AL117665	5912262	mRNA; cDNA DKFZp586M1824 (from clone DKFZp586M1824); partial cds /cds=(0,3671)	1	TGCATAGATGACCTTTGGATTATTGG ACTCTGACTATTGGGACCCTAAAT
7969	HUVEC cDNA	Hs.17428	AL133010	6453416	RBP1-like protein (BCAA), transcript variant 2, mRNA /cds=(466,4143)	1	TGGAGGCCCTAAGAAACAGAGAAAAAC AGAAATAACAACAGGAAGCTGCTT
7970	HUVEC cDNA	Hs.278242	AL137300	6807762	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2068,3421)	1	CAATAGCTTGTGGGTCTGTGAAGACT GCGGTGTTGAGTTTCTCACACCC
7971	HUVEC cDNA	Hs.7378	AL137663	6807784	mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227) /cds=UNKNOWN	1	TGCACTGTACTCTCTTCATAGGATTG TAAAGGTGTTCTAATCCAATTGCA
7972	HUVEC cDNA	Hs.61289	AL157424	7018453	mRNA; cDNA DKFZp761E1512 (from clone DKFZp761E1512) /cds=UNKNOWN	1	TGAAGTCATTTTCATTGGGAAGGAAAG CTGCAAGATTATTGGGGGACTAG
7973	HUVEC cDNA	Hs.240013	AL390148	9368882	mRNA; cDNA DKFZp547A166 (from clone DKFZp547A166) /cds=UNKNOWN	1	TTTCATCTGGCCACCCCTCCTTAGAC TCTCCTCCCTCAAGAGTTGGAGC
7974	HUVEC cDNA	Hs.22629	AW887820	8049833	602281231F1 cDNA, 5' end /clone=IMAGE:4368943 /clone_end=5'	1	GTGTAGAATTCCGATCCAGTCATCTC ACAGAACTTTCACACTAGGGTGCCA
7975	HUVEC cDNA	Hs.333414	BE562833	9806553	hypothetical protein MGC14151 (MGC14151), mRNA /cds=(108,485)	1	CGGACCCAGTTTCTTGTAACCAAGGG GGAAACATCGGGGACCCCAATGG
7976	HUVEC cDNA	NA	BE612847	9894444	601452239F1 NIH_MGC_66 cDNA clone IMAGE:3856304 5', mRNA sequence	1	TAAAGATGTCGGGTACACTTCGCCA AGGGTTAGCGTCTTTGGGCATTTTC
7977	HUVEC cDNA	Hs.86412	BE876332	10325018	chromosome 9 open reading frame 5 (C9orf5), mRNA /cds=(32,2767)	1	AACACAACACTAAACCGAACACACA CGTACTAACACACCCACGACCCAA
7978	HUVEC cDNA	Hs.285814	BE906669	10400012	sprouty (Drosophila) homolog 4 (SPRY4), mRNA /cds=(205,525)	1	CCTTCTGGTCTGCTTTTGACCAGCA TTTTTGTGCCCTCTGTTACTGTG
7979	HUVEC cDNA	Hs.113029	BF025727	10733439	ribosomal protein S25 (RPS25), mRNA /cds=(63,440)	1	GATATACGAAACACCACTGGACGA TGCGAAAAACGAGACGACATAAGC
7980	HUVEC cDNA	Hs.263339	BF107006	10889631	602377929F1 cDNA, 5' end /clone=IMAGE:4508646 /clone_end=5'	1	TGGACAGGCATGAAGGTTACAAATG GGAGAAAACACACACGTTATGT
7981	HUVEC cDNA	Hs.182426	BF204683	11098269	601867521F1 cDNA, 5' end /clone=IMAGE:4110052 /clone_end=5'	1	GCAGGAGAGCGAGAGAGGAGAAGAA GAGGCAGGAGGGAGAAAGAGCGTAC
7982	HUVEC cDNA	Hs.75968	BF217687	11111273	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(77,211)	1	CAAGAAGCAGAAGCAGCAACCAGAG ACAGAGAGACAAACGAGAACACA
7983	HUVEC cDNA	Hs.112318	BF237710	11151628	cDNA FLJ14633 fis, clone NT2RP2000938 /cds=UNKNOWN	1	AGAGGAAAGAATAGGACCAGTGCCG AGGTATAGGAGGAGGGGCATACTAA
7984	HUVEC cDNA	Hs.293981	BF247088	11162147	Homo sapiens, clone MGC:16393 IMAGE:3939021, mRNA, complete cds /cds=(506,1900)	1	TCGGAGTAAGGGCGATTGTCTCGTTA GGTAATACATCATCTTCGTGCATA

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7985	HUVEC cDNA	Hs.157850	BF303931	11250608	Homo sapiens, clone MGC:15545 IMAGE:3050745, mRNA, complete cds /cds=(1045,1623)	1	AGACAAGACGAGCAACGACAACCAC AGCAGCTCCATACACTCTGCCTCTC
7986	HUVEC cDNA	Hs.217493	D00017	219909	annexin A2 (ANXA2), mRNA /cds=(49,1058)	1	AGTGAAGTCTATGATGTGAACACTT TGCCCTCGTGTGATGTGTCATAA
7987	HUVEC cDNA	Hs.76549	D00099	219941	mRNA for Na,K-ATPase alpha-subunit, complete cds /cds=(318,3389)	1	TCACAAGACAGTCATCAGAACAGTA AATATCCGCTGCCAGTTCGATCA
7988	HUVEC cDNA	Hs.330716	D10522	219893	cDNA FLJ14368 fis, clone HEMBA1001122 /cds=UNKNOWN	1	AAACTCCTGCTTAAGGTGTCTAATT TCTGTGAGCACACTAAAAGCGAA
7989	HUVEC cDNA	Hs.75929	D21255	575578	mRNA for OB-cadherin-2, complete cds /cds=(476,2557)	1	CGTGCCAGATATAACTGTCTTGTTC AGTGAGAGACGCCCTATTCTATG
7990	HUVEC cDNA	Hs.178710	D21260	434760	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(172,5199)	1	TCCCTGAGGCTTGTGTATGTTGGATA TTGTGGTGTTTTAGATCACTGATG
7991	HUVEC cDNA	Hs.334822	D23660	432358	Homo sapiens, Similar to ribosomal protein L4, clone MGC:2988 IMAGE:3139805, mRNA, complete cds /cds=(1616,2617)	1	CAGAGAAGAACTACTACAGAGGA GAAGAAGCCTGCTGCATAAATCTT
7992	HUVEC cDNA	Hs.262823	D28500	7678803	hypothetical protein FLJ10326 (FLJ10326), mRNA /cds=(2,2296)	1	TCAGAACATAGATATGTATTCACTT GTCTTCAAATACGCCAAGCAGAA
7993	HUVEC cDNA	Hs.151761	D43947	603948	KIAA0100 gene product (KIAA0100), mRNA /cds=(329,6607)	1	TTGGGGTCAAGTGAAAGGGTAGGGG GATAGTCTGATCAAGTGTGATAAA
7994	HUVEC cDNA	Hs.699	D50525	1167502	peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA /cds=(21,671)	1	CAGCAAATCCATCTGAAGTGTGGAGG AGAAGCTCTCTTACTGAGGGTGC
7995	HUVEC cDNA	Hs.278607	D50911	6633996	mRNA; cDNA DKFZp434N0735 (from clone DKFZp434N0735); partial cds /cds=(0,1577)	1	CCTTCTCTTATGTGTGTAATCTGTA ATATACCATTCTCTGTGGCCTGT
7996	HUVEC cDNA	Hs.57729	D50922	1469186	Kelch-like ECH-associated protein 1 (KIAA0132), mRNA /cds=(112,1988)	1	GGATGGCACTTCCCCACCGGATGGA CAGTTATTTTGTGATAAGTAACCC
7997	HUVEC cDNA	Hs.240770	D59253	1060898	Homo sapiens, nuclear cap binding protein subunit 2, 20kD, clone MGC:4991 IMAGE:3458927, mRNA, complete cds /cds=(26,496)	1	TGAGTCAGTGTCTTACTGAGCTGGA AGCCTCTGAAAGTTATTAAGGCA
7998	HUVEC cDNA	Hs.155595	D63878	961447	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(258,1343)	1	CCCACACTGCTACACTTCTGATCCCC TTGGTTTTACTACCCAAATCTAA
7999	HUVEC cDNA	Hs.80712	D86957	1503987	sepin 2 (SEP2) mRNA, partial cds /cds=(0,1527)	1	GTGGCTTGCTAGTCTGTTACGTTAAC ATGCTTTTCTAAAATTGCTTCACG
8000	HUVEC cDNA	Hs.75822	D86970	1504013	mRNA for KIAA0216 gene, complete cds /cds=(484,5229)	1	TTGTACTCACTGGGCTGTGCTCTCCC CTGTTTACCCGATGTATGGAAATA
8001	HUVEC cDNA	Hs.170311	D89678	3218539	heterogeneous nuclear ribonucleoprotein D-like (HNRPL), transcript variant 1, mRNA /cds=(580,1842)	1	TTTATGATTAGGTGACGAGTTGACAT TGAGATTGTCTTTTCCCTGATC
8002	HUVEC cDNA	Hs.83213	J02874	178346	fatty acid binding protein 4, adipocyte (FABP4), mRNA /cds=(47,445)	1	TTGTTGTTTTCCCTGATTAGCAAGCA AGTAATTTTCTCCCAAGCTGATT
8003	HUVEC cDNA	Hs.177766	J03473	337423	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) (ADPRT), mRNA /cds=(159,3203)	1	TTAGAAACAAAAGAGCTTTCCTTCT CCAGGAATACTGAACATGGGAGCT
8004	HUVEC cDNA	Hs.155560	L10284	186522	calnexin (CANX), mRNA /cds=(89,1867)	1	CCATTGTTGTCAAATGCCAGTGTCC ATCAGATGTGTTCTCCATTCTTCT
8005	HUVEC cDNA	Hs.75693	L13977	431320	prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA /cds=(29,1519)	1	GATGTCTGGTGCCCAATGCCAGGAA GTGAGAGCCATTCTTTGTACTGG
8006	HUVEC cDNA	Hs.539	L31610	1220360	ribosomal protein S29 (RPS29), mRNA /cds=(30,200)	1	AGTTGGACTAAATGCTCTTCTTCAG AGGATTATCCGGGGCATCTACTCA
8007	HUVEC cDNA	Hs.1742	L33075	536843	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(467,5440)	1	TGAATTTACTTCTCCCAAGAGTTTG GACTGCCCGTCAGATTCTTCTGC
8008	HUVEC cDNA	Hs.180446	L38951	893287	importin beta subunit mRNA, complete cds /cds=(337,2967)	1	AAACACATACACAAAAACAGCAAAC TTCAGGTAACATATTTGGATTGCA
8009	HUVEC cDNA	Hs.79572	M11233	181179	cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA /cds=(2,1240)	1	CTGAGGATGAGCTGGAAGGAGTGAG AGGGGACAAAACCCACTTGTGGA
8010	HUVEC cDNA	Hs.273415	M11560	178350	aldolase A, fructose-bisphosphate (ALDOA), mRNA /cds=(167,1261)	1	TCTTCTTCCCTCGTGACAGTGGTGT GTGGTGTGCTGTGAATGCTAAG
8011	HUVEC cDNA	Hs.254105	M14328	182113	enolase 1, (alpha) (ENO1), mRNA /cds=(94,1398)	1	GCTAGATCCCGGTGGTTTTGTGCTC AAAATAAAAAGCCTCAGTGACCCA
8012	HUVEC cDNA	Hs.237519	M20867	183059	yz35c09.s1 cDNA, 3' end /clone=IMAGE:285040 /clone_end=3'	1	GCATGGCTTAACCTGGTGATAAAAGC AGTTATTAAAGTCTACGTTTTTCC
8013	HUVEC cDNA	Hs.1239	M22324	178535	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA /cds=(120,3023)	1	CCGCCCTGTACCTCTTTCACCTTTC CCTAAAGACCCTAAATCTGAGGAA
8014	HUVEC cDNA	Hs.118126	M22960	190282	protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA /cds=(6,1448)	1	GGACAGCCCCACAGGAGGTGGTGGA CGGACTGTAATTGATAGATTGATTA
8015	HUVEC cDNA	Hs.198281	M26252	338826	pyruvate kinase, muscle (PKM2), mRNA /cds=(109,1704)	1	ATTGAAGCCGACTCTGGCCCTGGCC CTTACTTGCTTCTAGCTCTCTAG

Table 8

8016	HUVEC cDNA	Hs.2050	M31166	339991	pentadn-related gene, rapidly induced by IL-1 beta (PTX3), mRNA /cds=(67,1212)	1	ACTAGACTTTATGCCATGGTGCTTTC AGTTTAATGCTGTGTCTCTGTCAG
8017	HUVEC cDNA	Hs.99853	M59849	182591	fibrillarin (FBL), mRNA /cds=(59,1024)	1	GAGCCATATGAAGAGACCATGCCGT GGTCGTGGGAGTGTACAGGCCACC
8018	HUVEC cDNA	Hs.283473	M64098	183891	hypothetical protein PRO2900 (PRO2900), mRNA /cds=(271,501)	1	ATAACAGACTCCAGCTCCTGGTCCAC CCGGCATGTCACTCAGCACTCTGG
8019	HUVEC cDNA	Hs.211573	M85289	184426	heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA /cds=(40,13221)	1	CTGGCCTCTGTCTCCTAGAAGGGAC CCTCCTGTGGTCTTTGTCTTGATT
8020	HUVEC cDNA	Hs.75103	M86400	189952	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA /cds=(84,821)	1	CCCAAAGCTCACTTTACAAAATATTTT CTCAGTACTTTGCAGAAAACACC
8021	HUVEC cDNA	Hs.59271	M96982	338262	U2(RNU2) small nuclear RNA auxiliary factor 1 (non-standard symbol) (U2AF1), mRNA /cds=(38,760)	1	ATGTCTGCTAGAAAGTGTGTAGTTG ATTGACCAAAACCACTTCATAAGGG
8022	HUVEC cDNA	Hs.110802	NM_000552	9257255	von Willebrand factor (VWF), mRNA /cds=(310,8751)	1	CTCTGCATGTTCTGCTCTTGTGCCCT TCTGAGCCCAACAATAAGGCTGAG
8023	HUVEC cDNA	Hs.274466	NM_001403	4503472	eukaryotic translation elongation factor 1 alpha 1-like 14 (EEF1A1L14), mRNA /cds=(620,1816)	1	TGCATCGTAAACCTTTTCAGAAAGGAA AGGAGAATGTTTTGTGGACACGTT
8024	HUVEC cDNA	Hs.279518	NM_001642	4502148	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	1	AGCCCTATTTCATGTCTCTACCCACTA TGCACAGATTAAACTTCACCTACA
8025	HUVEC cDNA	Hs.76224	NM_004105	9665261	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(149,1630)	1	AGTGACAGTGAACCTTAAGCAAATTAC CCTCTACCCAATTCTATGGAATA
8026	HUVEC cDNA	Hs.19545	NM_012193	6912383	frizzled (Drosophila) homolog 4 (FZD4), mRNA /cds=(306,1919)	1	ACACATGCCCTGAATGAATTGCTAAA TTTCAAAGGAAATGGACCTGCTT
8027	HUVEC cDNA	Hs.87125	NM_014600	7657055	EH-domain containing 3 (EHD3), mRNA /cds=(285,1892)	1	GCCACTGAACCAATCACTTTGTATGC TATGCTCCTACTGTGATGGAAAC
8028	HUVEC cDNA	Hs.119503	NM_016091	7705432	HSPC025 (HSPC025), mRNA /cds=(33,1727)	1	AGGACCGAAGTGTTCAGATGGAGTCT CAGTAAAGGATCTTTGGAGCCAGA
8029	HUVEC cDNA	Hs.7905	NM_016224	7706705	SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA /cds=(43,1830)	1	TTCAATGGAAAATGAGGGGTTTCTCC CCACTGATATTTTACATAGAGTCA
8030	HUVEC cDNA	Hs.283722	NM_020151	9910251	GTT1 protein (GTT1), mRNA /cds=(553,1440)	1	GCTCCATGTTCTGACTTAGGGCAATT TGATTCTGCACITGGGGTCTGTCT
8031	HUVEC cDNA	Hs.286233	NM_020414	14251213	sperm autoantigenic protein 17 (SPA17), mRNA /cds=(1210,1665)	1	GCAGCAGCTTAATTTTCTGTATTGC AGTGTATTATAGGCTTCTGTGTGT
8032	HUVEC cDNA	Hs.272822	S56985	298485	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACTTTGTCTGTACATACCTG GCCTCTGTGATTACATAGATCAGC
8033	HUVEC cDNA	Hs.279518	S60099	300168	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(72,2363)	1	AGCCCTATTTCATGTCTCTACCCACTA TGCACAGATTAAACTTCACCTACA
8034	HUVEC cDNA	Hs.194662	S80562	1245966	calponin 3, acidic (CNN3), mRNA /cds=(83,1072)	1	ACATGGAAGACTAAACTCATGCTTAT TGCTAAATGTGGTCTTTGCCAACT
8035	HUVEC cDNA	Hs.76669	U08021	494988	nicotinamide N-methyltransferase (NNMT), mRNA /cds=(117,911)	1	AGACCCCTGTGATGCCTGTGACCTCA ATTAAGCAATTCCTTTGACCTGT
8036	HUVEC cDNA	Hs.89857	U13991	562076	TATA box binding protein (TBP)-associated factor, RNA polymerase II, H, 30kD (TAF2H), mRNA /cds=(17,673)	1	CGCACTACTTCACTGAGCCACCCAA CCTAAATGTACTTATCTGTCCCCA
8037	HUVEC cDNA	Hs.1516	U20982	695253	insulin-like growth factor binding protein-4 (IGFBP4) gene, promoter and complete	1	CTGTAGACTCAGTGCCAGCCACAGCT TCAGAGATTGTGCTCATAGGTAT
8038	HUVEC cDNA	Hs.183648	U22816	930342	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (lirpin), alpha 1 (PPFIA1), mRNA /cds=(229,3837)	1	TGACAAAGGATTTTACGTTTATAAAAT TATGACAGAAGCCATGTGCCCCG
8039	HUVEC cDNA	Hs.83383	U25182	799380	thioredoxin peroxidase (antioxidant enzyme) (AOE372), mRNA /cds=(43,858)	1	GTCTGCCCTGCTGGCTGGAAACCTG GTAGTGAAACAATAATCCAGATCC
8040	HUVEC cDNA	Hs.75888	U30255	984324	phosphogluconate dehydrogenase (PGD), mRNA /cds=(6,1457)	1	CTCGTCATACAATGCCTGATGGGCTC CTGTCAACCCTCCACGTCTCCACAG
8041	HUVEC cDNA	Hs.169476	U34995	1497857	Homo sapiens, glyceraldehyde-3-phosphate dehydrogenase, clone MGC:10926 IMAGE:3628129, mRNA, complete cds /cds=(2306,3313)	1	CTAGGAGCCGCACCTTATCATGTAC CATCAATAAAGTACCCTGTGCTCA
8042	HUVEC cDNA	Hs.192023	U39067	1718194	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (EIF3S2), mRNA /cds=(17,994)	1	TCCGTATCCATTACTTCGACCACAG TACTTTGAATTTGAGTTTGAGGCT
8043	HUVEC cDNA	Hs.155637	U47077	13570016	DNA-dependent protein kinase catalytic subunit (DNA-PKcs) mRNA, complete cds /cds=(57,12443)	1	CCAGTCTCCACACCCAAACTGTTTC TGATTGGCTTTTGAAGCTTTTGTG
8044	HUVEC cDNA	Hs.285313	U51869	2745959	core promoter element binding protein (COPEB), mRNA /cds=(117,988)	1	CTGTTGTCTCTCTGAGGCTGCCAGTT GTTGTGTGTTACCGATGCCAGAAAG

Table 8

8045	HUVEC cDNA	Hs.184270	U56637	1336098	capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1), mRNA /cds=(0,860)	1	AATATAGTCAAGCAAGTTTGTTCAG GTGACCCATTGAGCTGTGTATGCA
8046	HUVEC cDNA	Hs.75064	U81234	1465773	tubulin-specific chaperone c (TBCC), mRNA /cds=(23,1063)	1	TTTGCTATTTTCGTATGCCTTTGAGA CTGAGTCTTACTCCGTCGCCAG
8047	HUVEC cDNA	Hs.183684	U73824	1857236	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA /cds=(308,3029)	1	TTGTGGGTGTGAAACAAATGGTGAGA ATTTGAATTGGTCCCTCCTATTAT
8048	HUVEC cDNA	Hs.165263	U89278	1877500	early development regulator 2 (homolog of polyhomeotic 2) (EDR2), mRNA /cds=(8,1309)	1	CAGGAAGGAGGTAGGCACCTTTCTG AGCTTATTCTATTTCCACCCACAC
8049	HUVEC cDNA	Hs.334703	W29012	1308969	Homo sapiens, clone IMAGE:3875338, mRNA, partial cds /cds=(0,930)	1	GGGAGCCATCCCTCTCTACCAAGGT GGCAATGATGGAGGGAACCTTGCATG
8050	HUVEC cDNA	Hs.287820	X02761	31396	mRNA for fibronectin (FN precursor) /cds=(0,6987)	1	TGGCCCGCAACTACTGTAGGAACAAG CATGATCTTGTACTGTGATATTTT
8051	HUVEC cDNA	Hs.143376	X04098	28338	actin, gamma 1 (ACTG1), mRNA /cds=(74,1201)	1	GGTTTCTACTGTTATGTGAGAACATT AGGCCCCAGCAACACGTCATTGT
8052	HUVEC cDNA	Hs.290070	X04412	35447	gelsolin (amyloidosis, Finnish type) (GSN), mRNA /cds=(14,2362)	1	AGCCCTGCAAAAATTCAGAGTCCTTG CAAAATTGTCTAAATGTGAGTGT
8053	HUVEC cDNA	Hs.79088	X06323	34753	mitochondrial ribosomal protein L3 (MRPL3), mRNA /cds=(76,1122)	1	TGGGGACTATAGTGCAACCTATTGG GTAAAGAAACCATTGTCTAAATG
8054	HUVEC cDNA	Hs.287797	X07979	31441	mRNA for FLJ00043 protein, partial cds /cds=(0,4248)	1	ACCACTGTATGTTTACTTCTCACCATT TGAGTTGCCCATCTTGTTCACA
8055	HUVEC cDNA	Hs.87409	X14787	37464	thrombospondin 1 (THBS1), mRNA /cds=(111,3623)	1	TTGACCTCCCATTTTACTATTGGCCA ATACCTTTTCTAGGAATGTGCT
8056	HUVEC cDNA	Hs.82202	X53777	34198	ribosomal protein L17 (RPL17), mRNA /cds=(288,840)	1	GAGGAGGTTGCCAGAGAAAGAAAGA TATCCAGAGAACTGAAGAAACA
8057	HUVEC cDNA	Hs.233936	X54304	34755	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA /cds=(114,629)	1	AACCTACCAGCCCTTCTCCCCAATA ACTGTGGGTCTATACAGAGTCAAT
8058	HUVEC cDNA	Hs.74405	X57347	32463	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(100,837)	1	AGAGAGTTGGACCACTATTGTGTGTT GCTAATCATTGACTGTAGTCCCAA
8059	HUVEC cDNA	Hs.77813	X59960	402620	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase) (SMPD1), mRNA /cds=(0,1889)	1	CCCTGTACTGCTGCTGCGACCTGATG CTGCCAGTCTGTTAAATAAAGAT
8060	HUVEC cDNA	Hs.172690	X62535	30822	diacylglycerol kinase, alpha (80kD) (DGKA), mRNA /cds=(103,2310)	1	ACACACATACACACACCCCAAAACAC ATACATTGAAAGTGCCCTCATCTGA
8061	HUVEC cDNA	Hs.272822	X63527	36127	RuvB (E coli homolog)-like 1 (RUVBL1), mRNA /cds=(76,1446)	1	ACCTCCCACTTTGCTGTGACTACTG- GCCTCTGTGATTACATAGATCAGC
8062	HUVEC cDNA	Hs.119529	X67698	37476	epididymal secretory protein (19.5kD) (HE1), mRNA /cds=(10,465)	1	AACAACATTAACTGTGGCCTCTTTCT- ACACCTGGAAATTTACTCTTGAA
8063	HUVEC cDNA	Hs.211579	X68264	433891	MUC18 gene exons 1&2 /cds=(26,1966)	1	TCTCTGCTCAATCTCTGCTTGCTCC AAGGACCTGGGATCTCTGGTACG
8064	HUVEC cDNA	Hs.75061	X70326	38434	macrophage myristoylated alanine-rich C kinase substrate (MACMARCKS), mRNA /cds=(13,600)	1	TGCTTACTCAAGTTCAAACTCCAG- CCTGTGAATCAACTGTCTCTTT
8065	HUVEC cDNA	Hs.31314	X72841	297903	retinoblastoma-binding protein 7 (RBBP7), mRNA /cds=(287,1564)	1	AACCTTTTACACTTTTCTTCCAACAC TTCTTGATTGGCTTTGCAGAAAT
8066	HUVEC cDNA	Hs.79088	X78669	469884	reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA /cds=(66,1019)	1	TGGTGAGTGAATTTGACATTGTCCA AACCTTTTTCATTTTGAGTGATT
8067	HUVEC cDNA	Hs.7957	X79448	2326523	adenosine deaminase, RNA-specific (ADAR), transcript variant ADAR-a, mRNA /cds=(187,3867)	1	GAGTGAGGAAGACCCCAAGCATAG ACTCGGGTACTGTGATGATGGCTGC
8068	HUVEC cDNA	Hs.76206	X79981	599833	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA /cds=(120,2474)	1	TGGCAAAGCCCTCACACTGCAAGG GATTGTAGATAACACTGACTTGT
8069	HUVEC cDNA	Hs.172182	Y00345	35569	poly(A)-binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(502,2403)	1	GGAAAGGAAACTTTGAACCTTATGTA CCGAGCAAATGCCAGGTCTAGCAA
8070	HUVEC cDNA	Hs.180414	Y00371	32466	hsc70 gene for 71 kd heat shock cognate protein	1	AGTTAAGATTATTCAGAAGGTGCGGG ATTGGAGCTAAGCTGCCACCTGGT
8071	HUVEC cDNA	Hs.75216	Y00815	34266	protein tyrosine phosphatase, receptor type, F (PTPRF), mRNA /cds=(370,6083)	1	TTACCTTGTGGATGCTAGTGCTGTAG AGTTCACTGTTGTACACAGTCTGT
8072	HUVEC cDNA	Hs.65114	Y07604	1945761	keratin 18 (KRT18), mRNA /cds=(51,1343)	1	GGGGTCTTCACATTATCATAACCTCT CCTCTAAAGGGGAGGCATTAATAA
8073	HUVEC cDNA	Hs.113503	Y08890	2253155	Homo sapiens mRNA for Ran_GTP binding protein 5 (RanBP5(Importin5) gene) /cds=(236,3529)	1	TTTCTTGTGCAATTGCAACTTAAAGC ATCGAGTTTTTACCATCTTCCACT
8074	HUVEC cDNA	Hs.44499	Y09703	4581482	pinin, desmosome associated protein (PNN), mRNA /cds=(30,2261)	1	ACATGTGCAATAAATGTGGCTTAGA CTTGTGTGACTGCTTAAGACTAAA
8075	HUVEC cDNA	Hs.8887	Y11307	2791897	cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA /cds=(80,1225)	1	AAATGTAGCTTTTGGGGAGGGAGGG GAAATGTAATCACTGGAATAATTGT

Table 8

8076	HUVEC cDNA	Hs.90061	Y12711	6759555	progesterone receptor membrane component 1 (PGRMC1), mRNA /cds=(78,665)	1	ACCCACTGCAAAAGTAGTAGTCAAGT GTCTAGGTCITTTGATATTGCTCTT
8077	HUVEC cDNA	Hs.101033	Y14391	6562622	Pseudoautosomal GTP-binding protein-like (PGPL), mRNA /cds=(329,1540)	1	GCCTGCTGTGAAGTGCCTTCCCTCGG AATGTTTCCGTAAACAGGACATTAA
8078	HUVEC cDNA	Hs.24322	Y15286	2584788	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 9kD (ATP6H), mRNA /cds=(62,307)	1	GAAGAGCCATCTCAACAGAATCGCAC CAAACATACITTCAGGATGAATT
8079	HUVEC cDNA	Hs.291904	Z31696	479156	accessory proteins BAP31/BAP29 (DXS1357E), mRNA /cds=(136,876)	1	AGGAGGGTGGGTGGAACAGGTGGAC TGGAGTTTCTCTTGAGGGCAATAAA
8080	HUVEC cDNA	Hs.180877	Z48950	761715	clone PP781 unknown mRNA /cds=(113,523)	1	TGCTTGATTAGATGCCATAATAGTG CTGTATTTGCAGTGTGGGCTAAGA
8081	HUVEC cDNA	Hs.289101	Z49835	860985	glucose regulated protein, 58kD (GRP58), mRNA /cds=(0,1517)	1	TTGGGGGAAATGTTGTGGGGGTGGG GTTGAGTTGGGGGTATTTTCTAATT
8082	HUVEC cDNA	Hs.10340	AK000452	7020548	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(334,1170)	1	AGCATGGTAAACCTGGGTTTTGTTC TATTTTCTCCAGACAGAAATGCAA
8083	HUVEC cDNA	Hs.194676	AK001313	7022490	tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), transcript variant 2, mRNA /cds=(827,4488)	1	GGTCTCTTTGACTAATCAACAAAG CAACCACTTAGCCAGTTTTATT
8084	HUVEC cDNA	Hs.808	AK001364	7022577	heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570)	1	GCCCTTGATGCTGGAGTCACATCTGT TGATAGCTGGAGAAGCTTTAGTTTC
8085	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ11349 fis, clone PLACE4000650, weakly similar to TUBERIN /cds=UNKNOWN	1	GCCGATTCCAGCGAGGGATTTAATC CTTACATTTTGCCCATTTGGCTC
8086	HUVEC cDNA	Hs.29692	AK021498	10432693	cDNA FLJ11438 fis, clone HEMBA1001213 /cds=UNKNOWN	1	TTCCCTGGACAGTTTGTATGTGCTTAT GGTTGAGATTATTAATCTGCTTGT
8087	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds /cds=(128,1129)	1	GGCGGTGACTGCCCCAGACTTGGTT TTGTAATGATTGTACAGGAATAAA
8088	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (EC 2.4.1.41) /cds=(418,1791)	1	TGACCATTTGGAGGGGCGGGGCTC CTAGAAGAACCTTCTTAGACATGG
8089	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds=UNKNOWN	1	CAGTCCTCACACCAGCCAAGGTACACA GGCAAGAGCAAGAAGAGAACTGA
8090	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CCTCAGTGATGGAATATCATGAATGT GAGTCATTATGTAGCTGTCTGATACA
8091	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds=(81,1055)	1	ACACACAACCTCAGCTTTGCATCAG AGTCTTGATTCCAAAGAAATCAA
8092	HUVEC cDNA	Hs.322680	AK025200	10437664	cDNA: FLJ21547 fis, clone COL06206 /cds=UNKNOWN	1	GGAATTTGCGACCAGAGGACCCACC ACGTCCTCGCTCGACATCTTGAAC
8093	HUVEC cDNA	Hs.288061	AK025375	10437878	actin, beta (ACTB), mRNA /cds=(73,1200)	1	GGAGGCGCCAGGGCTTACCTGTAC ACTGACTTGAGACCAGTTGAATAAA
8094	HUVEC cDNA	Hs.288869	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	CAGAGAAAGAAAGGCAAAAGACTG GTTTGTTCCTTAATTTCTTCTGT
8095	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337)	1	GAAAGCAGGGAAGCAGTGTGAACCTC TTTATTCACCTCCAGCCTGTCCCTGT
8096	HUVEC cDNA	Hs.334842	AK026632	10439528	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(67,1422)	1	TGGTTAGATTGTTTCACTTGGTGAT CATGTCTTTTCCATGTGTACCTGT
8097	HUVEC cDNA	Hs.288036	AK026650	10439548	tRNA isopentenylpyrophosphate transferase (IPT), mRNA /cds=(80,1040)	1	TGCATCGTAAACCTTCAGAAAGGAAA GGAGAATGTTTGTGGACCACTT
8098	HUVEC cDNA	Hs.324406	AK026741	10439662	ribosomal protein L41 (RPL41), mRNA /cds=(83,160)	1	TGGACCTGTGACATCTGGACTATTT CTGTGTTTATTTGTGGCCGAGTGT
8099	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(68,319)	1	TGCAACTAGCAACTCATCTTCGGAAG ACACAGCCAGGAGAATGAAGTAGA
8100	HUVEC cDNA	Hs.289071	AK027187	10440255	cDNA: FLJ22245 fis, clone HRC02612 /cds=UNKNOWN	1	GACTTTCTCTCTGCGAGCTTCTACT TCTAAGTCTGAATCCAGTCAGAAA
8101	HUVEC cDNA	Hs.334788	BG385658	13278634	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689)	1	GTTTCTCTTTGGTTTTCCAGATTTTCT TTAGAACGGTGACTGACCCTCCT
8102	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	CTGAGCAATAACTAGCATAACCCCTT GGGGCCTCTAAACGGGTCTTGAGG
8103	HUVEC cDNA	NA	U07360	476289	Human DXS1178 locus dinucleotide repeat polymorphism sequence zc09e02.s1 cDNA, 3' end /clone=IMAGE:785978 /clone_end=3'	1	TGCCCCATTTACATTGCTCATTACTCA TGCAAAATTTCTCTTGCTAACCT
8104	HUVEC cDNA	Hs.230165	AA449779	2163529		1	ACCCACCATTTGGTAAATATTACAGG GAACCTTGTTTAAAGTTTATGCT

Table 8

8105	HUVEC cDNA	NA	AI000459	3191013	ot07c08.s1 NCI_CGAP_GC3 cDNA clone IMAGE:1614158 3' similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUM	1	GTCAAATAAGGTTGTTCTTTCCTTGAA GGACAGCACCCATGCCACAGCAC
8106	HUVEC cDNA	Hs.172922	AI016204	3230540	ot83f03.s1 cDNA, 3' end /clone=IMAGE:1623389 /clone_end=3'	1	CTGGAAAAACATCACATGGTTGAGTC AAGGATGAAAAGTCAAACCTACCT
8107	HUVEC cDNA	Hs.96457	AI081571	3418363	ox59h10.s1 cDNA, 3' end /clone=IMAGE:1660675 /clone_end=3'	1	ATCCATCCAATAAACACAGCAACACC CTATGCTACTGACCAAGCAAAGCT
8108	HUVEC cDNA	NA	AI082318	3419110	ox72c08.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:1661870 3' similar to gb:X63527 60S RIBOSOMAL PROTEIN	1	TAGTTAGAGTCCAAGACATGGTTCCT CCCCCTTTGTCTGTACATCCTGGC
8109	HUVEC cDNA	Hs.145222	AI187426	3738064	qf31d08.x1 cDNA, 3' end /clone=IMAGE:1751631 /clone_end=3'	1	CAGCCTGCCTGCTTGCCATTTTTCTT CCCCTTCCATTTTTCTAACCTCAG
8110	HUVEC cDNA	Hs.273194	AI285483	3923716	ty56b02.x1 cDNA, 3' end /clone=IMAGE:2283051 /clone_end=3'	1	ACTTCCTCCCCCTCCCCCTAGCATT CTTATATGATATGTTTCCATACCC
8111	HUVEC cDNA	Hs.238797	AI307808	4002412	602081661F1 cDNA, 5' end /clone=IMAGE:4245999 /clone_end=5'	1	AAGGAATTTGTTTTCCTATCCTAACT CAGTAACAGAGGGTTTACTCCGA
8112	HUVEC cDNA	Hs.135872	AW028193	5886949	wv61h08.x1 cDNA, 3' end /clone=IMAGE:2534079 /clone_end=3'	1	TTTGCATCCCGAGTTTGTATTCCAA GAAAATCAAAGGGGGCCAATTTGT
8113	HUVEC cDNA	Hs.244816	AW078847	6033999	xb18g07.x1 cDNA, 3' end /clone=IMAGE:2576700 /clone_end=3'	1	AAACAGGAAGGGGTTTGGGCCCTT TGATCAACTGGAACCTTTGGATCAAG
8114	HUVEC cDNA	Hs.249883	AW162315	6301348	au66d07.x1 cDNA, 3' end /clone=IMAGE:2781229 /clone_end=3'	1	AAAAACGGTTTATGGGGGTAGGGAAA CAGGCCGAAAAGAACGTGGAGAAA
8115	HUVEC cDNA	Hs.329930	AW170757	6402282	xj24e07.x1 cDNA, 3' end /clone=IMAGE:2658180 /clone_end=3'	1	GGGGACTCAGGCCCCGCTGGGGGT CCCACATAGGGTTTTATCCAAAAA
8116	HUVEC cDNA	Hs.23349	AW237511	6569800	nab70e03.x1 cDNA, 3' end /clone=IMAGE:3273292 /clone_end=3'	1	TGTTGTTGGATACGTACTTAAGTGGT ATGCATCCCATGTCTTTGGGTACT
8117	HUVEC cDNA	NA	BE672733	10033274	7b75g07.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3234108 3' similar to TR:O99231 O99231 CYTOCHROME OXIDASE	1	TGAGAGCACACCATAAATTCACAGCA GGAATAAACGAAGACACACGAGCA
8118	HUVEC cDNA	Hs.288443	BF110312	10940002	7n36d08.x1 cDNA, 3' end /clone=IMAGE:3566654 /clone_end=3'	1	ACCAGGGCTTAAACCTCAATTTATG TTCATGACAGTGGGGATTTTTCTT
8119	HUVEC cDNA	Hs.111301	J03210	180670	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase) (MMP2), mRNA /cds=(289,2271)	1	AGCCATAGAAGGTGTTCAAGTATTGC ACTGCCAACTCTTTGTCCGTTTTG
8120	HUVEC cDNA	Hs.82085	M14083	189566	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA /cds=(75,1283)	1	CCATGCCCTTGTCATCAATCTTGAAT CCCATAGCTGCTTGAATCTGCTGC
8121	HUVEC cDNA	Hs.80120	Y10343	2292903	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(31,1710)	1	TTAAGAATGTGGCAGAAATGTATGCT GAGGTAGCCAGTCAATCCTTATT
8122	HUVEC cDNA	Hs.10340	AK000452	7020548	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(334,1170)	1	ATCAGTAGCAAAACAAACCCAGCAAC TTCTGTCCAGCATCTGCTGTAGGG
8123	HUVEC cDNA	Hs.73742	AK001313	7022490	cDNA FLJ10451 fis, clone NT2RP1000959, highly similar to acidic ribosomal phosphoprotein P0 mRNA /cds=UNKNOWN	1	CCCATCTAACTAGCACACGAACCTTC CACGAGGACGCTGGCGAGAGAAG
8124	HUVEC cDNA	Hs.808	AK001364	7022577	heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA /cds=(323,1570)	1	GAACTTGGCAGTTGTAGCAGAGGCA GTTGAGGCTTGTTGACCATCACCAT
8125	HUVEC cDNA	Hs.15978	AK002211	7023952	cDNA FLJ111349 fis, clone PLACE4000650, weakly similar to TUBERIN /cds=UNKNOWN	1	CGCTCTCTCTGCACAGCACCACCAC CAACAGTCTGGATGATTTTAGGCA
8126	HUVEC cDNA	Hs.29692	AK021498	10432693	cDNA FLJ11438 fis, clone HEMBA1001213 /cds=UNKNOWN	1	TTTTGGGAAGAAAACCCATATGCATCT GAAATACAATTTGGCAATGGAAGCT
8127	HUVEC cDNA	Hs.109672	AK023900	10435975	Homo sapiens, Similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) F, clone MGC:14252 IMAGE:4128833, mRNA, complete cds /cds=(128,1129)	1	CTCTTTGTTGCTACTCATTTCTCTCCG GCGTCTGCTGAGGGGTAGGTGTC

Table 8

8128	HUVEC cDNA	Hs.25635	AK024039	10436304	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) /cds=(418,1791)	1	CAACTTCCTCTTGGTTACCCAGAAGA ACAGCAGCACCGTGATCCAGAGCA
8129	HUVEC cDNA	Hs.288967	AK024167	10436481	cDNA FLJ14105 fis, clone MAMMA1001202 /cds=UNKNOWN	1	CTGTACATCTGCATCCCAGCAAAGAG CAGCAGGGACAGGAGGGAGGAGAG
8130	HUVEC cDNA	Hs.25001	AK024230	10436557	cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to mRNA for 14-3-3gamma /cds=UNKNOWN	1	CACAGACAGAAGGTTTCGTTCTCAT TCGACAGTGGCTCATTACAGCTCTG
8131	HUVEC cDNA	Hs.6101	AK025006	10437439	hypothetical protein MGC3178 (MGC3178), mRNA /cds=(81,1055)	1	TCAAGATTGGCAATTCAGTGTGCCCA TTAAACCACTCAGTAGCTCAGCCT
8132	HUVEC cDNA	Hs.322680	AK025200	10437684	cDNA: FLJ21547 fis, clone COL06208 /cds=UNKNOWN	1	AGTTGTCTCTGAGAGTTTTACACTTGT GAGAAAACTACTGGCAGCTTTGATT
8133	HUVEC cDNA	Hs.288061	AK025375	10437878	actin, beta (ACTB), mRNA /cds=(73,1200)	1	CACATAGGAATCCTCTGACCCATTGC CCACCATCAGCCCTGGTGCCTGG
8134	HUVEC cDNA	Hs.288869	AK025842	10438480	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(342,1586)	1	AACAGGAACCTTTATCTCTTTGTGAG GCGATTGCACTTCCACACAGGC
8135	HUVEC cDNA	Hs.251653	AK026594	10439481	tubulin, beta, 2 (TUBB2), mRNA /cds=(0,1337)	1	GTAATTGCCGCCGGTGGCCTCATTGT AGTACACGTTGATGCGTTCAGCT
8136	HUVEC cDNA	Hs.278242	AK026632	10439528	Homo sapiens, clone MGC:3214 IMAGE:3502620, mRNA, complete cds /cds=(2066,3421)	1	ATAGTGGCTAGGGATTAGGAGGCGA AGGCGACAGGAGCAGACACCGGGCTC
8137	HUVEC cDNA	Hs.181165	AK026650	10439548	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(53,1441)	1	CATTTTGGCTTTTAGGGGTAGTTTTC ACGACACCTGTGTTCTGGCGGCAA
8138	HUVEC cDNA	Hs.108124	AK026741	10439662	cDNA: FLJ23088 fis, clone LNG07026 /cds=UNKNOWN	1	CCCTGGTTCAGGAATTAAGGGGACA GACTTGAATAAGAAACAAACAAAA
8139	HUVEC cDNA	Hs.274368	AK026775	10439706	MSTP032 protein (MSTP032), mRNA /cds=(68,319)	1	ACAGTAGAGAATTTGAGTACACAGGG TATGGAGAGTAGGGCACAAAATGT
8140	HUVEC cDNA	Hs.241507	AK027187	10440255	cDNA: FLJ23534 fis, clone LNG06974, highly similar to HUMRPS6A ribosomal protein S6 mRNA /cds=UNKNOWN	1	GAACAGCCTCGTCTTTCCCGGAATGC CAGGCAGGATGACGATGAACGTGG
8141	HUVEC cDNA	Hs.334788	BG392671	13286119	hypothetical protein FLJ14639 (FLJ14639), mRNA /cds=(273,689)	1	GACCTCCAGAATTCCTCATCGCTGT CGGTGACCAAGTCCACAGACACTA
8142	HUVEC cDNA	NA	NC_002090	9507429	many cloning vectors, kanamycin resistance, gene	1	TCTTGCCATCCTATGGAAGTGCCTCG GTGAGTTTTCTCCTTCATTACAGA
8143	HUVEC cDNA	NA	U07360	476289	Human DXS1178 locus dinucleotide repeat polymorphism sequence	1	TGTTACTCCTTCAAGCCCCTGAATCA CTATAGCCACGACTCTCCAATGA

TABLE 9: Cardiac Transplant patient RNA samples and array hybridizations

Patient #	Sample	Rejection Grade	RNA Yield (μ g)	Hybridization #
14-0001	1			
	2	3A	13.6	107739
	3	1A	5.83	107740
14-0002	1			
	2			
	3			
14-0003	1	0	12.8	
	2			
	3			
14-0004	1			
	2			
14-0005	1	3A	1.08	107741
	2	0	11.2	107742
	3			
	4			
14-0006	1	2	2.02	
	2			
	3			

TABLE 10: Differentially expressed probes between samples from patients with high and low grade rejection:

Oligo#	Gene Represented
7401	cDNA clone IMAGE:915561
1796	amphiregulin
4423	partial IGVH3 gene for immunoglobulin heavy chain V region
4429	partial IGVL1 gene for immunoglobulin lambda light chain V region
4430	partial IGVH3 DP29 gene for immunoglobulin heavy chain V region
4767	cDNA clone COL09252, highly similar to CD24
4829	oncostatin M
8091	mRNA for a predicted protein

We claim:

1. A system for detecting gene expression comprising at least two isolated DNA molecules wherein each isolated DNA molecule detects expression of a gene wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO:1 - SEQ ID NO: 8143.
2. The system of claim 1 wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO: 2283, SEQ ID NO:6025, SEQ ID NO: 4481, SEQ ID NO:3761, SEQ ID NO: 3791, SEQ ID NO:4476, SEQ ID NO: 4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO: 4429, SEQ ID NO:4430, SEQ ID NO: 4767, SEQ ID NO:4829, and SEQ ID NO: 8091.
3. The system of claim 1 wherein the DNA molecules are synthetic DNA, genomic DNA, PNA or cDNA.
4. The system of claim 1 wherein the isolated DNA molecules are immobilized on an array.
5. The system of claim 4 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
6. A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecules of claim 1.
7. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to nucleic acid derived from the RNA and c) hybridizing said nucleic acid derived from the RNA to the isolated DNA molecules of claim 1.
8. The method of claim 7 wherein said nucleic acid derived from the RNA is cDNA.

9. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to the isolated DNA molecules of claim 1.
10. A candidate library comprising at least two isolated oligonucleotides wherein the oligonucleotides have nucleotide sequences having at least 40-50, 50-60, 70-80, 80-85, 85-90, 90-95 or 95-100% sequence identity to the nucleotide sequences selected from the group consisting of SEQ ID NO:1- SEQ ID NO: 8143.
11. The candidate library of claim 10, wherein the nucleotide sequence comprises deoxyribonucleic acid (DNA) sequence, ribonucleic acid (RNA) sequence, synthetic oligonucleotide sequence, protein nucleic acid (PNA) sequence or genomic DNA sequence.
12. The candidate library of claim 11, wherein the candidate library is immobilized on an array.
13. The candidate library of claim 12, wherein the array is selected from the group consisting of: a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
14. A diagnostic oligonucleotide for a disease comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 - SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual with at least one disease criterion for at least one leukocyte-related disease compared to the expression of said gene in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.
15. The diagnostic oligonucleotide of claim 14, wherein the nucleotide sequence comprises DNA, cDNA, PNA, genomic DNA, or synthetic oligonucleotides.

16. The diagnostic oligonucleotide of claim 14, wherein the disease criterion comprises data wherein the data is selected from physical examination data, laboratory data, patient historic, diagnostic, prognostic, risk prediction, therapeutic progress, and therapeutic outcome data.
17. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise peripheral blood leukocytes or leukocytes derived from a non-blood fluid.
18. The diagnostic oligonucleotide of claim 17, wherein the non-blood fluid is isolated from the colon, sinus, esophagus, small bowel, pancreatic duct, biliary tree, ureter, vagina, cervix uterus, nose, ear, urethra, eye, open wound, abscess, stomach, cerebral spinal fluid, peritoneal fluid, pleural fluid, synovial fluid, bone marrow and pulmonary lavage.
19. The diagnostic oligonucleotide of claim 14, wherein the leukocytes comprise leukocytes derived from urine or a biopsy sample.
20. The diagnostic oligonucleotide of claim 14, wherein the leukocytes are peripheral blood mononuclear cells or T-lymphocytes.
21. The diagnostic oligonucleotide of claim 14, wherein the disease is selected from the group consisting of cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus (SLE), rheumatoid arthritis, osteoarthritis, and cytomegalovirus infection.
22. The diagnostic oligonucleotide of claim 14, wherein the differential expression is one or more of: a relative increase in expression, a relative decrease in expression, presence of expression or absence of expression.
23. A diagnostic agent comprising an oligonucleotide wherein the oligonucleotide has a nucleotide sequence selected from the group consisting of SEQ ID NO:1 - SEQ ID NO: 8143 wherein said oligonucleotide detects expression of a gene that is differentially expressed in leukocytes in an individual over time.

24. The agent of claim 23 wherein said oligonucleotide is selected from the group consisting of SEQ ID NO:2476, SEQ ID NO: 2407, SEQ ID NO:2192, SEQ ID NO:2283, SEQ ID NO:6025, SEQ ID NO:4481, SEQ ID NO:3761, SEQ ID NO:3791, SEQ ID NO:4476, SEQ ID NO:4398, SEQ ID NO:7401, SEQ ID NO: 1796, SEQ ID NO:4423, SEQ ID NO:4429, SEQ ID NO:4430, SEQ ID NO:4767, SEQ ID NO:4829, and SEQ ID NO:8091.

25. A diagnostic probe set for a disease comprising at least two probes wherein each probe detects expression of a gene wherein the gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1 - SEQ ID NO:8143 wherein each gene is differentially expressed in leukocytes in an individual with at least one disease criterion for a disease selected from Table 1 as compared to the expression of the gene in leukocytes in an individual without the at least one disease criterion, wherein expression of the gene is correlated with the at least one disease criterion.

26. An isolated nucleic acid wherein said nucleic acid comprises a sequence depicted in SEQ ID NO:8144 - SEQ ID NO:8766.

27. An expression vector containing the nucleic acid of claim 26 in operative association with a regulatory element which controls expression of the nucleic acid in a host cell.

28. A host cell comprising the expression vector of claim 27.

29. The host cell of claim 27, wherein the host cell is a prokaryotic cell or a eukaryotic cell.

30. A kit comprising the system of claim 1.

31. A system for detecting gene expression in leukocytes comprising an isolated DNA molecule wherein said isolated DNA molecule detects expression of a gene wherein said gene is selected from the group of genes corresponding to the oligonucleotides depicted in SEQ ID NO: 1-SEQ ID NO: 8143 and said gene is differentially expressed in said leukocytes in an individual with at least one disease

criterion for a disease selected from Table 1 compared to the expression of said gene in leukocytes in an individual without the at least one disease criterion.

32. The system of claim 31 wherein the DNA molecule is at least 16 nucleotides in length.
33. The system of claim 31 wherein the DNA molecules are synthetic DNA, genomic DNA, PNA or cDNA.
34. The system of claim 31 wherein the isolated DNA molecule is immobilized on an array.
35. The system of claim 34 wherein the array is selected from the group consisting of a chip array, a plate array, a bead array, a pin array, a membrane array, a solid surface array, a liquid array, an oligonucleotide array, polynucleotide array or a cDNA array, a microtiter plate, a membrane and a chip.
36. A method of detecting gene expression comprising a) isolating RNA and b) hybridizing said RNA to the isolated DNA molecule of claim 31.
37. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to nucleic acid derived from the RNA and c) hybridizing said nucleic acid derived from said RNA to the isolated DNA molecules of claim 31.
38. The method of claim 37 wherein said nucleic acid derived from the RNA is cDNA.
39. A method of detecting gene expression comprising a) isolating RNA; b) converting said RNA to cRNA or aRNA and c) hybridizing said cRNA or aRNA to the isolated DNA molecule of claim 31.
40. A method of diagnosing a disease comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31 and comparing the expression of the gene with a molecular signature indicative of the presence or absence of said disease.

41. A method of monitoring progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.

42. A method of monitoring the rate of progression of a disease comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease progression.

43. A method of predicting therapeutic outcome comprising: obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the predicted therapeutic outcome.

44. A method of determining prognosis for a patient comprising obtaining a leukocyte sample from a patient, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene, and comparing the expression of the gene with a molecular signature indicative of the prognosis.

45. A method of predicting disease complications in an individual comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of disease complications.

46. A method of monitoring response to treatment in an individual, comprising obtaining a leukocyte sample from an individual, contacting said leukocyte sample with the gene expression system of claim 31, and comparing the expression of the gene with a molecular signature indicative of the presence or absence of response to treatment.

47. The method according to claim 46, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

48. The method according to claim 41, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

49. The method according to claim 42, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

50. The method according to claim 43, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

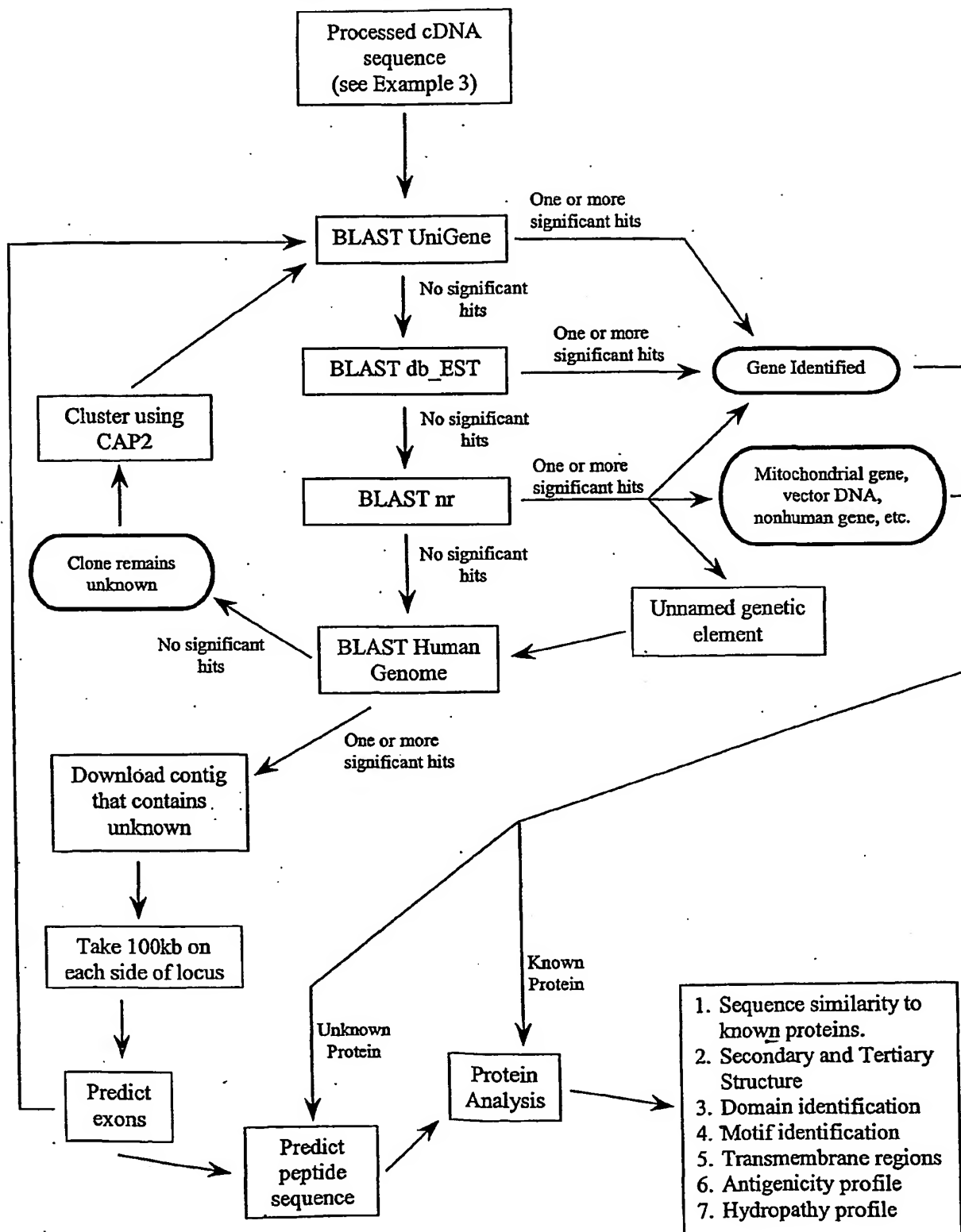
51. The method according to claim 44, wherein said method further comprises characterizing the genotype of the individual, and comparing the genotype of the individual with a diagnostic genotype, wherein the diagnostic genotype is correlated with at least one disease criterion.

52. The method of claim 50, wherein the genotype is analyzed by one or more methods selected from the group consisting of Southern analysis, RFLP analysis, PCR, single stranded conformation polymorphism, and SNP analysis.

53. A method of RNA preparation suitable for diagnostic expression profiling comprising: obtaining a leukocyte sample from a subject, adding actinomycin-D to a final concentration of 1 ug/ml, adding cycloheximide to a final concentration of 10 ug/ml, and extracting RNA from the leukocyte sample.

54. The method of claim 52, wherein the actinomycin-D and cycloheximide are present in a sample tube to which the leukocyte sample is added.

Figure 1: Novel Gene Sequence Analysis



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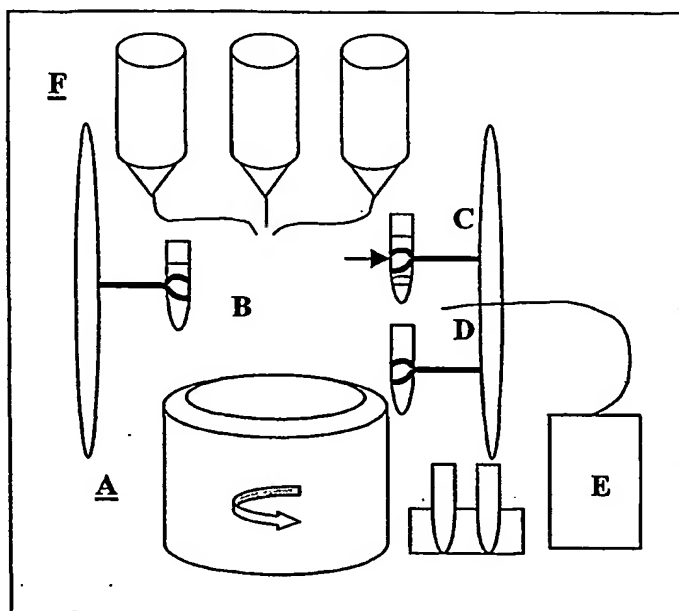
Figure 2 . Automated Mononuclear Cell RNA Isolation Device

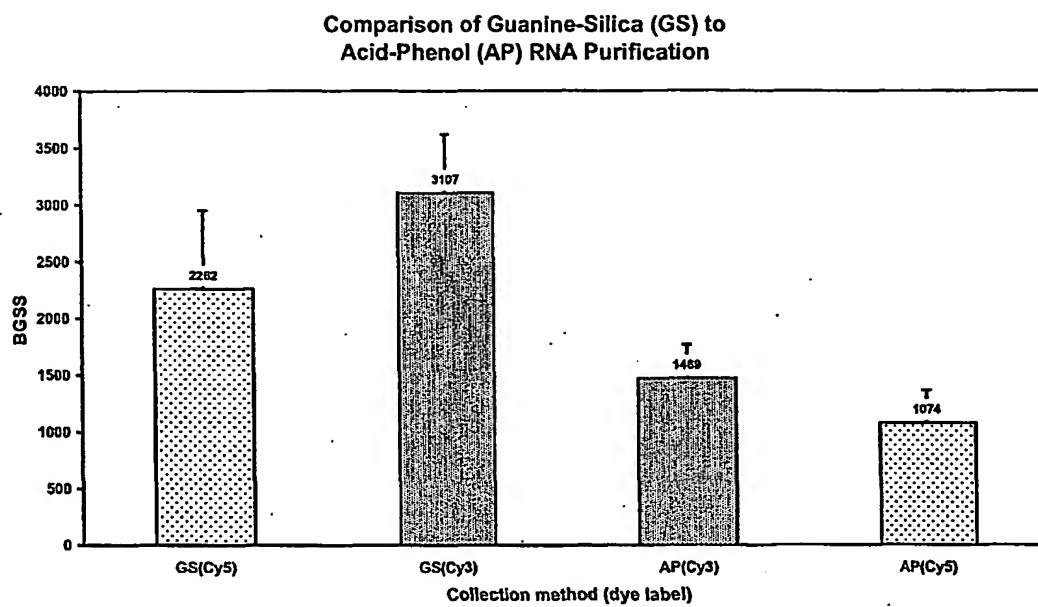
Figure 3: Kits for discovery of, or application of diagnostic gene sets**A. Contents of kit for discovery of diagnostic gene sets**

1. Sterile, endotoxin and RNase free blood collection tubes (>10cc capacity)
2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
3. Erythrocyte lysis buffer
4. Leukocyte lysis buffer
5. Substrates for labeling of RNA (may vary for various expression profiling techniques)
 - For fluorescence cDNA microarray expression profiling:
 - Reverse transcriptase and 10x RT buffer
 - Poly-dT primer
 - DTT
 - Deoxynucleotides 100mM each
 - RNase inhibitor
 - Cy3 and Cy5 labeled deoxynucleotides
6. cDNA microarrays containing candidate gene libraries
7. Cover slips for slides
8. hybridization chambers
9. Software package for identification of diagnostic gene set from data
 - Contains statistical methods.
 - Allows alteration in desired sensitivity and specificity of gene set.
 - Software facilitates access to and data analysis by centrally located database server.
10. Password and account number to access central database server.
11. Kit User Manual

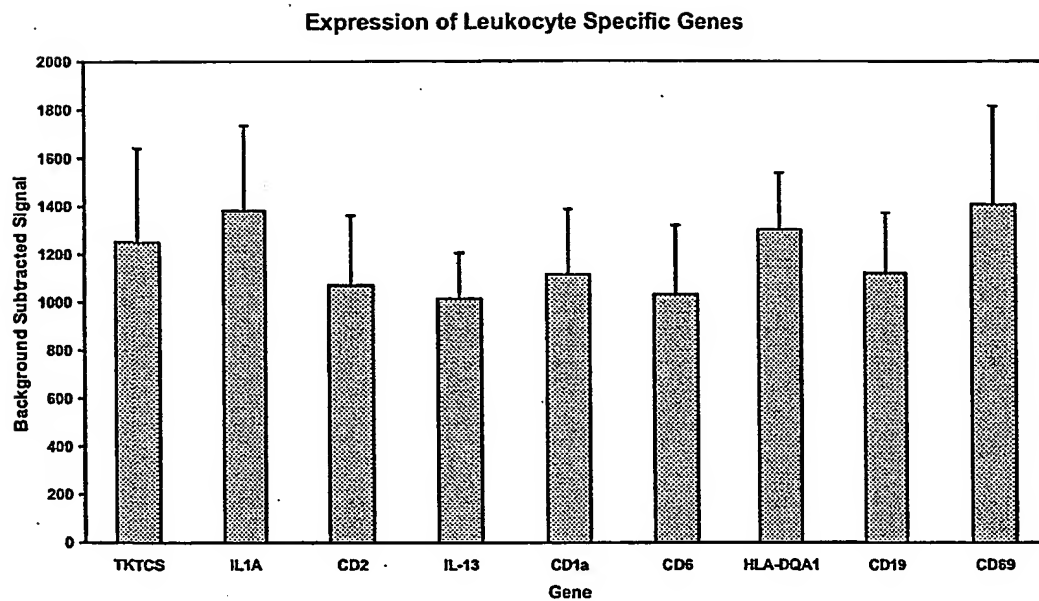
B. Contents of kit for application of diagnostic gene sets

1. Sterile, endotoxin and RNase free blood collection tubes (>10cc capacity)
2. Alcohol swabs, tourniquet, 18g needle and syringe (>10cc capacity)
3. Erythrocyte lysis buffer
4. Leukocyte lysis buffer
5. Substrates for labeling of RNA (may vary for various expression profiling techniques)
 - For fluorescence cDNA microarray expression profiling:
 - Reverse transcriptase and 10x RT buffer
 - Poly-dT primer
 - DTT
 - Deoxynucleotides 100mM each
 - RNase inhibitor
 - Cy3 and Cy5 labeled deoxynucleotides
6. cDNA microarrays containing diagnostic gene sets
7. cover slips for slides
8. hybridization chambers
9. Software package for identification of diagnostic gene set from data
 - Contains statistical methods.
 - Allows alteration in desired sensitivity and specificity of gene set.
 - Software facilitates access to and data analysis by centrally located database server
10. Password and account number to access central database server.
11. Kit User Manual

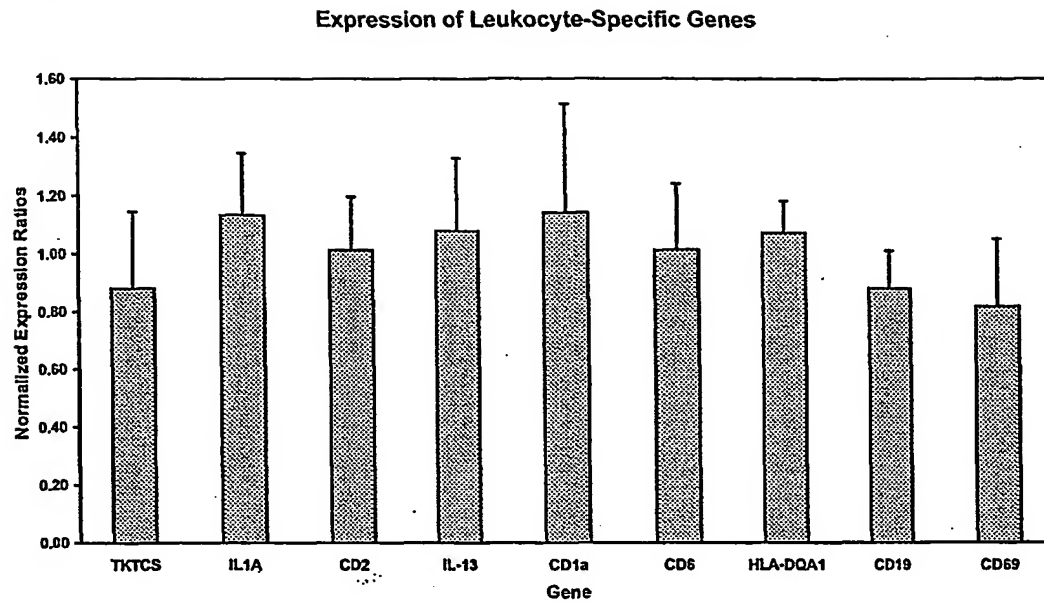
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Figure 4

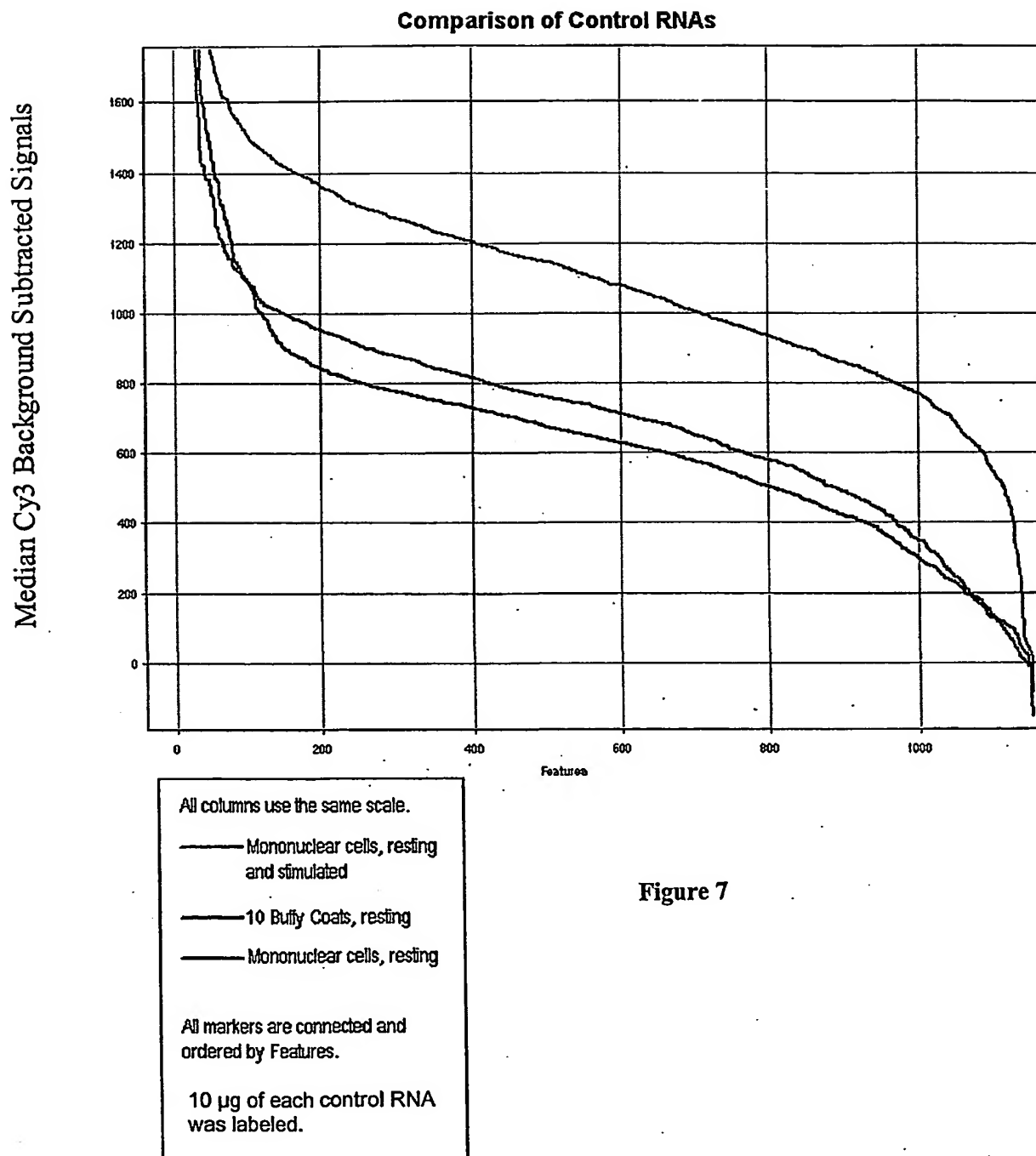
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**Figure 5**

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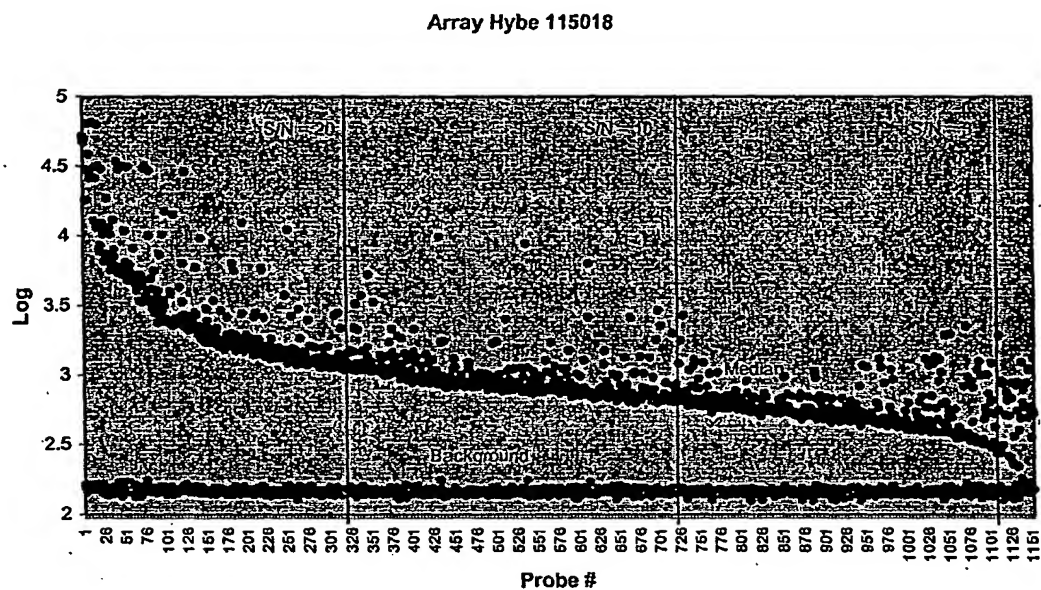
Figure 6

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**Figure 7**

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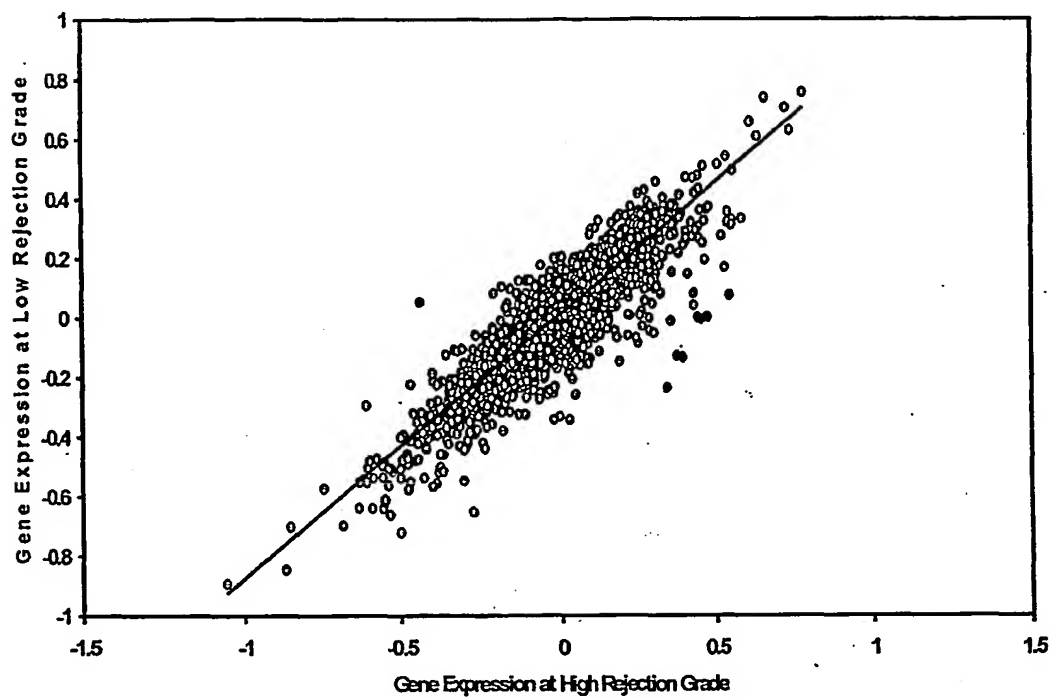
Figure 8: Log expression of each probe using the R50 reference RNA. Probe expression is ordered by Signal to noise, S/N, decreasing from left to right.



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Figure 9

Comparison of High Rejection Grade to Low Rejection Grade



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Figure 10: Differential gene expression between grade 0 and 3A samples:

Probe			Array 107742: Grade 0				Array 107739: Grade 3A				Ratio of SRs	
Acc #	Name	Oligo ID	F633 Median - S632	F532 Median - S532	Cy3/Cy5 Ratio	SR: scaled ratio (gr)	F633 Median - S632	F532 Median - S532	Cy3/Cy5 Ratio	SR: scaled ratio (gr)	Grade 0/3A	Grade 3A/0
NM_003202	transcription factor 7 (T-cell specific, HMG-box) (TCF7)	2476	5558	1050	0.188917	0.710038	5927	358	0.061438	0.219793	3.23048873	0.30955069
BE220969	major histocompatibility complex, class II, DQ beta 1 (HL	6025	1810	635	0.350829	1.318579	2150	252	0.117209	0.419312	3.14482275	0.31800317
BE220969	major histocompatibility complex, class II, DQ beta 1 (HL	6025	1402	487	0.347361	1.305545	2121	247	0.116455	0.416612	3.13371958	0.31910959
NM_002922	regulator of G-protein signalling 1 (RGS1), mRNA /cds=	2407	804	85	0.118159	0.444098	1884	75	0.035809	0.142415	3.11833431	0.32068403
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6	2192	4121	405	0.098277	0.369371	7385	254	0.034394	0.123043	3.00195843	0.33311587
NM_002341	lymphotxin beta (TNF superfamily, member 3) (LTB), tr	2283	13488	3447	0.255556	0.960516	29882	2727	0.091259	0.326476	2.94207495	0.33989617
BE220969	major histocompatibility complex, class II, DQ beta 1 (HL	6025	1539	515	0.334633	1.257707	1942	237	0.122039	0.436591	2.88074502	0.34713223
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6	2192	3850	398	0.10025	0.376823	7705	282	0.0368	0.130934	2.87796556	0.34746767
U05040	ter upstream element (FUSE) binding protein 1 (FUBP1	3581	4507	1119	0.24828	0.933154	2390	220	0.09205	0.329308	2.83369583	0.35289603
X14008	nuclear receptor subfamily 4, group A, member 2 (NR4A	3729	1365	167	0.122344	0.459827	6541	434	0.045488	0.162731	2.82568319	0.35389672
NM_003202	transcription factor 7 (T-cell specific, HMG-box) (TCF7)	2476	2716	486	0.17894	0.672539	5310	356	0.067043	0.239845	2.80405488	0.3566264
AF035947	cytokine-inducible inhibitor of signalling type 1b mRNA,	642	9850	5254	0.533401	2.004771	969	197	0.203302	0.727307	2.75642938	0.36270818
NM_001781	CD69 antigen (p60, early T-cell activation antigen) (CD6	2192	3357	356	0.108047	0.398574	5963	246	0.041254	0.147586	2.70062725	0.37028503
Y14737	mRNA for immunoglobulin lambda heavy chain /cds=(85	4905	1390	248	0.178417	0.670576	6581	5767	0.878982	3.144527	0.21325167	4.68929496
Y14737	mRNA for immunoglobulin lambda heavy chain /cds=(85	4905	1398	240	0.171674	0.845231	7159	8112	0.853751	3.054262	0.21125576	4.73359883
BC006402	mRNA for immunoglobulin lambda heavy chain /cds=(85	4481	1826	295	0.161555	0.6072	2973	2498	0.840229	3.005889	0.20200364	4.95040578
X57812	rearranged immunoglobulin lambda light chain mRNA /c	3761	6512	747	0.114711	0.431139	27381	17730	0.847529	2.316513	0.19611538	5.37301111
X57812	rearranged immunoglobulin lambda light chain mRNA /c	3761	6728	755	0.112218	0.421766	28820	18636	0.846534	2.313311	0.18232143	5.48481857
X72475	cDNA: FLJ21321 fls, clone COL02335, highly similar to	3790	8572	1188	0.138591	0.520889	17322	13892	0.801986	2.869076	0.18155283	5.50803866
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X72475	cDNA: FLJ21321 fls, clone COL02335, highly similar to	3791	11974	1559	0.130115	0.489034	24281	18781	0.773299	2.768449	0.17677319	5.65896846
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AF067420	SNCT73 protein (SNCT73) mRNA, complete cds /cds=(39	4399	2654	243	0.09156	0.344125	37518	21610	0.57599	2.060585	0.16700357	5.98789603
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BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4474	7538	684	0.09074	0.341044	6038	4037	0.698599	2.391889	0.14258368	7.01342553
BC002963	rearranged immunoglobulin mRNA for mu heavy chain e	4474	8662	780	0.090048	0.338444	4339	2975	0.685642	2.45286	0.13797951	7.24745312
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Wohlgemuth, Jay
Quertermous, Thomas
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Phillips, Julie
Woodward, Robert
Ly, Ngoc
Altman, Peter

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